Targeting Osteosarcoma heterogeneity to improve therapeutic response

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Highlights

- Distinct transcriptomic states were identified in osteosarcoma cell lines using single-cell RNA sequencing.
- Lineage tracing identified states with differential sensitivity to therapy.
- Using perturb-seq, we identified transcription factors that drive cells towards a more sensitive state.
- The transcription factors NR0B1 and NFE2L3 were identified as targets capable of reprogramming cells to a sensitive state.

Summary

Intra tumor heterogeneity complicates cancer therapy by providing tumors with the ability to alter their phenotypes and become more therapy resistant. Here, we tested the hypothesis that identifying and modulating expression of key state-specific transcription factors could be used as a strategy for driving cells to a more therapy-sensitive state. Recent single-cell studies have explored the inter and intra tumoral heterogeneity of osteosarcoma and identified gene pathways enriched in specific cell states. For example, metastatic tumors are characterized by an expression of genes in the TNF-α, PI3K, TGFß and mTOR pathways. We identified similar profiles in osteosarcoma patient-derived xenograft-derived cell lines and potential transcription factor drivers of these states. We then used perturb-seq to downregulate expression of key transcription factors and evaluated the effect of these modulations on single cell RNA profiles and drug responses. Knockdown of *NFE2L3* or *NR0B1* increased the proportion of cells sensitive to targeted therapy. This approach, which could potentially be applied to other cancers, could be used as a strategy to increase the response to targeted therapies by increasing the proportion of cells in a drug-sensitive state.

Introduction

Intra-tumor heterogeneity and cell plasticity pose major challenges to successfully targeting cancer.[1,2] Intra-tumor heterogeneity, which can be inferred from the existence of distinct transcriptional states within a single tumor, results in varying phenotypic responses to therapy. This phenomenon allows some cancer cells to adapt or survive upon treatment, leading to relapse and progression despite initial treatment responses. Cellular plasticity is another therapeutic hurdle as it provides cells the ability to rapidly adapt in response to treatment. Osteosarcoma (OS), a bone cancer most commonly found in children and young adults, exemplifies these challenges, particularly in cases involving metastatic disease.[3,4]

Targeted therapies for OS have so far proven mostly ineffective, particularly for patients who present with metastasis.[5] Highly toxic chemotherapy, specifically Cisplatin, Doxorubicin and Methotrexate, has been the standard of care for over 40 years.[6,7] Targeting TFs that regulate cellular heterogeneity may be a potential approach for modulating multiple molecular pathways regulating a resistant phenotype in OS and other cancers.[2,8,9] Recent studies have explored the complexity of intratumoral OS heterogeneity using single-cell sequencing and cell-state transition modeling, identifying states and pathways associated with relapse and metastasis.[10,11] For example, OS metastases are enriched for pathways including TGF-ß, VEGFA, PI3K/AKT and mTOR.[11,12] However, it remains unclear how modulating these pathways changes state proportion of cells in different states, which is critical for addressing compensatory mechanisms.

In this study, we show similarities between cell states within PDX-derived OS cell lines and published single-cell RNA-seq data of primary samples. For example, both the PI3K/AKT/mTOR and VEGFA pathways are enriched in a subset of cells in PDX-derived cell lines. While inhibiting these pathways alone have been found to improve therapeutic efficacy,[13,14] we sought to identify key transcriptional drivers of these cell states, in order to mitigate the compensatory effects of specific pathway inhibition. To this end, we first identified therapy-sensitive cell-states using lineage tracing. After identifying a sensitive transcriptomic state in OS PDX-derived cell lines, we tested whether perturbing lineage drivers modulated the proportion of cells in the sensitive state. Inhibiting expression of *NFE2L3* or *NR0B1* increased the proportion of cells in a therapeutically sensitive state in OS PDX-derived cell lines, providing proof-of-principle for this approach.

Results

Osteosarcoma PDX-derived cell lines are characterized by three states

PDX samples have transcriptional profiles similar to those of the primary tumors from which they were derived.[15] We previously developed a panel of OS PDX-derived cell lines from osteosarcoma PDXs that have been well characterized with regards to genomic and phenotypic features. The bulk transcriptomes of these lines are highly correlated with that of the primary tumor.[16] We used three of these cell lines (OS152, OS384 and OS742) derived from metastatic, resected and diagnostic samples respectively to study intra sample heterogeneity as a therapeutic hurdle in OS. OS152 and OS742 both have amplifications of *MYC* while OS384 has a *VEGFA* amplification **(Figure S1A)**. Both *MYC* and *VEGFA* amplifications have been previously associated with metastasis and relapse in OS.[17,18]

These three cell lines were analyzed using single-cell RNA sequencing (scRNA-seq).[19] 6,490 (OS152), 3,244 (OS384), and 4,766 (OS742) single-cell transcriptomes were successfully generated for these cell lines **(Figure S1B and Methods)**. Using leiden clustering, we identified 5 clusters (populations of transcriptionally similar cells) for each cell line **(Figure 2A)**. We then reduced these initial clusters to 3 three groups using non-negative matrix factorization to decompose the data into 3 components **(Figure 1A, 2B-C and Methods)**. Differential gene expression analysis (DGEA) on the groups, which were assigned state names “A”, “B” and “C”, revealed state-specific gene markers. For example, *COL1A1* and *S100A6* were identified as markers for State “A”, *CENPF* and *UBE2C* for State “B” and *FTH1* and *PSMB6* for State “C” **(Figure 2D)**. State specific markers were then filtered to keep those that appeared in two or more of the samples **(Table 1)**. We also used GSEA to identify pathways enriched in each state. For example, this confirmed enrichment of TGF-ß, PI3K/AKT/mTOR and VEGFA pathways in State “A” **(Figure 2E)**. The genes and pathways enriched in State “A” have previously been associated with metastatic and recurrent OS tumors.[11] We also found that the State “A” had higher rates of cells within the G1 cell-cycle phase **(Figure S2A)**. State “B”, on the other hand, enriched for the CSR and GCNP pathways while State “C” enriched for the ESC pathway **(Figure 2E)**. This analysis supports the existence of transcriptionally similar subpopulations across the samples and suggests the likelihood that there is significant transcriptional heterogeneity within tumors.

To strengthen our confidence in the transcriptional similarities between samples, we performed label transfer between samples in a more unbiased fashion (see methods). This process entailed training an encoder model on the State labels from one sample and predicting the State labels within another sample. In doing so, we found that a high proportion of cells within the test data that were predicted to be of a certain state were originally labeled that state based on enriched pathways and markers **(Figure S2B)**. The use of this predictive model on the entire transcriptome profiles supported the presence of the three previously identified states. The training and validation loss curves were plotted to ensure minimal overfitting and convergence **(Figure S3A)**. To evaluate the precision and recall of the model trained on every sample dataset, we also computed the F1 scores **(Figure S3B)**. These findings further support the recurring transcriptomic patterns within the selected OS cell lines.

Lineage tracing identifies state with increased sensitivity to therapy in OS PDX-derived cell lines

Having defined the transcriptional similarity within subpopulations present within the OS PDX-derived cell lines, we sought to determine whether the three identified states had variable sensitivity to specific drugs. To enable the identification of sensitive clones after performing scRNA-seq at baseline, we used a barcode library containing barcodes that, upon transduction, are both integrated into the genomic DNA and expressed as part of the 3' UTR of BFP.[20] Detection of the same barcodes in both genomic DNA and scRNAseq libraries allows for the analysis of barcode frequencies after different therapeutic conditions using the gDNA and simultaneously enables association of barcoded cells to specific transcriptomic phenotypes. Using this approach, we explored the variable sensitivity of cell states within the OS PDX-derived cell lines at a single-cell resolution.

Transduced cells were sorted followed by plating at low density to downsize the total number of recovered barcodes to approximately 1,000 **(Figure S4A)**. Cells were then treated with one of three drugs i) Cisplatin, a ii) CDK 4/6 inhibitor or iii) ATR inhibitor **(Figure 3A)**. Cisplatin was used because it is part of the chemotherapy standard of care for OS.[14] Both CDK-4/6 and ATR inhibitors have been previously tested in OS, but found to have variable efficacy.[21,22] Thus we hypothesized they would be useful agents to evaluate the hypothesis that modulation of cell state could increase sensitivity to these agents.

After treatment with one of these three drugs, we harvested the genomic DNA from the treated and control replicate sets and amplified the lineage tracing barcodes **(Figure 3A; see Methods)**. We could then ensure that there were adequate counts for each replicate **(Figure S5A)** and compute correlations of each replicate to assess experimental precision **(Figure S5B and S1A)**. After plotting the count distributions, we found that certain barcodes contained far higher counts, suggestive of increased replicative capacity compared to other clones **(Figure S5C)**. We then plotted the ranked barcodes and filtered the dataset based on average log for the time 0 technical replicates **(Figure S5D)**. This analysis ensured that we were using high-quality counts within our analysis and provided a whitelist with which to filter the datasets from other time points and treatment conditions.

We then identified enriched and depleted barcodes by taking the log fold change of the counts per million (cpm) values between the treated and control samples. For example, OS052 had higher rates of depleted and enriched barcodes with more than 200 depleted and more than 80 enriched barcodes for both the ATR-inhibitor treatment and CDK-4/6 inhibitor **(Figure 3C)**. In OS384, on the other hand, we identified 61 depleted and 37 enriched barcodes for the CDK-4/6 treatment, 50 depleted and 33 enriched barcodes for the Cisplatin treatment and 45 depleted and 30 enriched for ATR treatment, suggesting variable clonal sensitivity to this therapy (**Figure 3C)**. Finally, OS742 had 66 depleted and 45 enriched barcodes for CDK-4/6 treatment **(Figure 3C)**. After comparing the depleted barcode overlap for different treatment combinations in OS384, we found that a significant proportion of barcodes were commonly depleted in different treatments **(Figure 3D)**. These findings support the hypothesis that the progeny of individual cells have differential sensitivity to therapy. Identification of the depleted and enriched barcodes would also help inform sensitive states within the cell lines after performing scRNA-sequencing on another control replicate set.

After performing scRNA-sequencing on the control replicate set **(Figure S6A)**, targeted PCR-enrichment and sequencing of the barcode-carrying BFP transcripts allowed for mapping of the lineage tracing barcodes to the associated cell-barcodes. This allowed us to identify which cluster

each of the enriched and depleted lineage tracing barcodes belonged to, enabling the comparison of the proportions of depleted barcodes within all cells for each state and the proportion of depleted barcodes within the rest of the cells. After designating clusters with the correct State assignment **(Figure 3B)**, we could infer if cells within a given state demonstrated higher rates of sensitization to each drug. For OS384 and OS742, we found State “B” contained higher likelihoods of containing depleted barcodes (OS384: Odds ratio of 1.62 for CDK4-6 i treatment, 2.36 for ATR treatment and 1.75 for Cisplatin treatment) **(Figure 3E)**. However, we also found that State “A” barcodes had a higher likelihood of being depleted for OS052 (Odds ratio of 2.93 for ATR-i and 2.55 for CDK 4/6-i treatment) **(Figure 3E)**. These findings suggest that State “B” transcriptomic profile is associated with the sensitive phenotype in OS384 and OS742 and helped identify States “A” and “C” as the states to target for reprogramming to improve therapy sensitivity.

Identifying State drivers

Although several pathways, such as the VEGFA and mTOR pathways, have been identified as potential targets to enhance therapeutic efficacy in OS,[6,23,24] compensatory mechanisms can reintroduce a resistant phenotype after inhibiting these pathways.[13] To address the limitations posed by these compensatory mechanisms, we focused on modulating cell states rather than targeting individual pathways. In doing so, we aimed to increase the proportion of cells in the sensitive state by inhibiting transcription of suspected drivers for the less sensitive states **(Figure 4A)**.

Having identified State “B” as potentially a more sensitive population **(Figure 3E)**, we sought to identify TFs that could regulate the transition to cell states **(Figure 1C)**. We identified candidate regulators of these states using CellRank. CellRank utilizes the theories of state transition and trajectory inference to infer potential drivers of a specific lineage.[25] Recently, various tools have been released to model state transitions and trajectories with pseudotime, a unit-less time measurement.[26] For example, after modeling gene expression through pseudotime for the State “A” trajectory, we found that *CSAG1* and *CD40* were expressed early on within the trajectory while *IGSF3* was expressed later on within the trajectory **(Figure 4B)**. Genes that are enriched early on within one trajectory relative to others may serve as drivers for the respective trajectories.

Having identified terminal states using CellRank **(Figure 4C)**, we could then identify candidate drivers for the terminal states by correlating expression of genes with fate probabilities for a given terminal state. Using this approach, we identified 10 candidate transcription factor candidate drivers, *DDIT3, TSHZ2, STAT1, NR0B1, NFE2L3, TCF4, NFKB2, IRF1, ZIC2* and *KLF12* **(Figure 4D, 4E, S7A and S7B)**.

To complement this analysis, we used MAVE to infer TFs suspected of regulating State “A”. MAVE is designed to capture regulatory interactions by integrating biological knowledge into its neural network architecture, representing regulatory interactions between TFs and their regulated genes with edges in the first two layers of an encoder. After inputting the State “A” gene markers, we identified transcription factors *JUN, JUNB, DDIT3*, *CEBPB* and *FOS* as potential drivers for State “A” in multiple samples (**Figure S7C**). *DDIT3*, *CEBPB* and *FOS* were predicted to regulate State “A” in three cell lines while *JUNB* was predicted to regulate State “A” in two cell lines. These transcription factors are associated with poor prognosis in other cancers, suggesting that they could also contribute to the

resistant phenotype observed in OS State “A”.[27,28] In total, we identified 12 suspected transcription factor lineage regulators to further investigate **(Table 2)**. We then wanted to determine whether targeting these TFs could reprogram cells toward the more sensitive phenotype.

Reprogramming cells to sensitive state and testing efficacy of top targets

The 12 transcription factors identified as suspected drivers were knocked down using the Perturb-seq pipeline which enables the combination of pooled screens with scRNA-seq to simultaneously capture the guide-RNA and associated transcriptome.[29] After transducing OS384, OS742 and OS833 with the dCas9-KRAB m-Cherry and the dual-guide RNA (gRNA) constructs,[30,31] we sorted the successfully transduced cells for both mCherry and BFP expression **(Figure S8A)**. Sorted cells were cultured for 72 hours and used to generate scRNA-seq libraries with the 10X platform **(Figure 5A)**.

After analyzing this scRNA-seq dataset and confirming proper knockdown of TFs **(Figure S9B and S9C)**, we identified which perturbations increased the proportion of cells in each state. To do so, we filtered the datasets based on quality control parameters **(Methods and Figure S8B)** and quantified changes in state proportions for each perturbation. Upon comparing the proportion of cells within each cluster between the target and the non-targeting control, we found that targeting *NFE2L3* in OS384 was most effective at increasing the proportion of cells in the cluster enriching for the State “B” module, which was previously associated with elevated sensitivity **(Figure 5B and 5C)**.

To integrate the data from all three samples into a single analysis, we used a binary logistic regression model to predict the likelihood of cells being in State “B” based on the transcription factor that was targeted with the cell line variable used as a covariate. We found that both *NFE2L3* or *NR0B1* knock-downs resulted in higher likelihoods of cells being in State “B” while reducing the likelihood of being in State “A”. JUN and IRF1 perturbations also reduced the likelihood of cells being in State “A” and increased the likelihood of cells being in State “C” **(Figure 5E)**. Both targets have previously been associated with resistance in a variety of cancers. *NFE2L3* was found to promote radiotherapy resistance in esophageal squamous cell carcinoma while *NR0B1* has recently been found to promote resistance in both hepatocellular carcinoma (HCC) and lung cancer.[32–34] NR0B1 was also found to mediate resistance by inhibiting apoptotic pathways and inducing autophagy pathways or c-JUN and NRF2. Interestingly, JUN was also identified as a target in our analysis. NFE2L3, on the other hand, was found to regulate resistance via the *IL-6* pathway.

We then tested treatment sensitivity after knocking down these targets with the dCas9/CRISPRi system. *NFE2L3* KD and control cells were treated with Cisplatin, an ATR inhibitor and a CDK 4/6 inhibitor with the same 15-day drug regimen used in the lineage tracing experiment and viability was quantified using the CellTiterGlo assay. *NFE2L3* KD improved the efficacy of the ATR inhibitor in both OS384 and OS833 but had no effect on the sensitivity to the CDK-4/6 inhibitor. Surprisingly, KD of NFE2L3 seemed to decrease the sensitivity to cisplatin **(**$p = 0.003$, t-test, **Figure 5F)** . We found no differences in the growth rates between the *NFE2L3* KD and control cells **(Figure 5D)**. To explore the potential mechanisms for this phenotype, we also explored the downstream modulated genes after *NFE2L3* knockdown. Knockdown of *NFE2L3* resulted in downregulated expression of *TGFß1* and *KIF1A* **(Figure S9C)**, potential mechanisms for sensitization within these samples. TGF-ß, for example, has been identified as a compensatory mechanism for BRAF, EGFR and HER2

inhibition.[35,36] Target genes for NFE2L3 were also downregulated in NFE2L3 KD cells suggesting that the NFE2L3 regulome was effectively modulated **(Figure S9D)**.

Discussion

Heterogeneity and compensatory mechanisms remain two of the most difficult challenges for successful treatment of various cancers. Osteosarcoma (OS), an aggressive pediatric cancer characterized by early metastasis and significant treatment resistance, demonstrates these same challenges.[38] The survival rate for patients with metastatic OS remains below 30%.[39] Resistance to targeted therapy in OS and many other cancers is likely due to extensive intratumor heterogeneity and the activation of compensatory survival pathways.[11,40,41] These hurdles underscore the importance of studying resistance from a systems perspective by assaying entire transcriptomic states.[5,20] Several pathways, including mTOR, TGF-ß, and VEGFA, have been previously implicated in OS resistance, many of which are particularly enriched in metastatic cells, exacerbating the treatment challenges and contributing to the poor survival rates observed in patients with metastatic disease.[43] In fact, pathways such as TGF-ß has been recognized in so many cancers as promoting angiogenesis and suppressing anti-tumor immunity, that various groups have developed ways to inhibit TGF-ß.[44] Our study represents a shift in this paradigm by identifying and targeting cellular states rather than individual pathways, thereby offering a more systematic approach to combating resistance.

We identified three states within the OS PDX-derived cells lines and the sensitive state using a lineage tracing approach. We identified State “B” as the likely more sensitive state. After identifying and perturbing suspected drivers for the specific states using the perturb-seq pipeline, we found that *NFE2L3* or *NR0B1* KD resulted in higher likelihoods of cells being in State “B”. *NFE2L3* has previously been identified as a potential target in Bladder Cancer and hepatocellular carcinoma which promotes cell proliferation.[45,46] We also found that *NFE2L3* KD was able to sensitize the OS PDX-derived cell lines to an ATR inhibitor, but not to cisplatin or a CDK-4/6 inhibitor. In fact, the *NFE2L3* KD seemed to make the cells more resistant to cisplatin.

Using this strategy, we show how intra-sample heterogeneity can be analyzed to identify targets capable of shifting an increased proportion of cancer cells to a sensitive state. We were able to modulate multiple pathways at once and reduce the likelihood of compensatory pathways reintroducing resistance — a common problem in Osteosarcoma and other cancers. This approach could be used to improve the efficacy of various emerging therapies including immunotherapies.[47]

While individual perturbations like knocking down *NFE2L3* or *NR0B1* have demonstrated potential in shifting cells towards a sensitive state in our study, it is increasingly evident that combinatorial perturbations may yield more robust outcomes for reprogramming purposes.[48] The underlying rationale is that by targeting multiple transcription factors, it is possible to interfere with the compensatory mechanisms that often undermine the efficacy of single-agent therapies.

However, the exploration of combinatorial perturbations introduces significant challenges, due to increasing costs with the vast number of potential combinations. To address this, recent tools offer promising avenues for predicting the outcomes of multi-target perturbations without the need for

exhaustive empirical testing. Tools such as CPA, CellOracle, and GEARS have shown efficacy in simulating transcriptomic changes post-perturbation, enabling the identification of potentially efficacious combinations.[49,50]

By integrating these tools into our research pipeline, we can systematically explore the combinatorial landscape, effectively narrowing down the options to those most likely to induce a reprogrammed, sensitive state in osteosarcoma cells. Moreover, novel constructs capable of delivering multiple gRNAs in a single intervention have recently been introduced and can further enhance the practical applicability of these combinatorial approaches,[51] paving the way for the modulation of even more pathways simultaneously and perhaps further improving therapeutic efficacy in various cancers.

Limitations of the Study

A major limitation of this study may be the inherent plasticity of the cells, allowing them to transition to a more resistant state after a therapeutic inhibitor degrades. This limitation could perhaps be addressed by the use of multiple doses or the gradual release of the therapeutic agent for a more consistent inhibition of the target. Efficacy improvements may also be mitigated by the gradual induction of compensatory mechanisms, necessitating longitudinal studies to identify resistance mechanisms that arise after a given amount of time.

Although this approach successfully reprogrammed a large proportion of the cells, we may be able to reprogram a larger proportion by targeting TFs that might reprogram cells out of terminal states as well. Despite these limitations, the approach taken in this study may provide a foundation for sensitizing tumor cells to existing or novel therapies.

Reagents table

Reagent or Resource	Company	ISBN/Cat. number
DMEM medium	Gibco	
Agilent tapestation reagents	Avantor	76645-270
TransIT-293 Transfection Reagent	Mirus Bio	MIR 2705
DNeasy Blood and Tissue Kit	Qiagen	57205964
10X kit 3’ V3.1	10X Genomics	1000268
PBS pH 7.4 (1X)	Gibco	
DNA clean and concentrator	Zymo research	D4014
One Shot™ Stbl3™ Chemically Competent E. coli	Thermo Fisher Scientific	C737303
White walled, clear bottom 96-well plate	Greiner	655098

Cell Titer Glo	Promega	G9241
Elimusertib (BAY-1895344) hydrochloride (ATR inhibitor)	Selleckchem	S8666
Q5 Hot Start hifi master 2X master mix	New England Biolabs	M0494S
Zymoclean Gel DNA Recovery KIT	Zymo research	D4007

Methods

Cell Cultures
The OS PDX-derived cell lines OS052, OS152, OS384, OS742 and OS833 were used for the experiments in this study and were originally derived from PDX models.[52] The cell lines were generated by implanting patient Osteosarcoma (OS) tumor cells in mice and then culturing the cells from the resected mouse tumors.[17] The cell lines were cultured for less than 13 passages in DMEM +Glutamine (Gibco) with 5% FBS and Penicillin-Streptomycin. HEK293T cells were also cultured in DMEM +Glutamine (Gibco) with 5% FBS and Penicillin-Streptomycin. All cells were kept in a 37 °C and 5 % humidified CO_2 incubator.

Single-cell RNA sequencing, quality control and read-alignment
10X scRNA-seq libraries were prepared with the v3.1 kit. Prior to GEM preparation, 10,000 cells were prepared in cold PBS and loaded onto a Next GEM chip before being loaded onto the 10X Chromium X. After reverse transcription, the cDNA libraries were amplified for 11 cycles, analyzed on the Agilent Tapestation and quantified on the Qubit before being sequenced on the Novaseq machine. The single-cell RNA sequencing FASTQ files were then processed using Cell Ranger version-7 with default settings. The “feature-reference” argument was used for the Perturb-seq data to assign lineage tracing barcodes and gRNAs respectively to individual cells. Cellsorted-possorted bam files were then generated with Samtools to be used by velocyto to generate loom files.[53]

After creating an anndata object from the loom files with Scanpy, the data was filtered based on the number of genes, total counts and mitochondrial percentage before being regressed on mitochondrial percentages and ccdifference scores. The ccdifference scores were computed by taking the difference between the G2M and S phase scores which were generated by quantifying enrichment of G2 and S gene lists with the Scanpy ‘score_cell_cycle_genes’ command.[54]

Prior to umap generation, dimensionality reduction and clustering were performed with PCA and the leiden algorithm, respectively. Prior to assigning clusters to states, we aggregated the clustered datasets from the different samples, We then computed the average expression for each cluster and gene and normalized that data using z-score normalization. We could then aggregate the different clusters using non-negative matrix factorization (NMF), assigning clusters to one of the 3 groups based on the dominant component weights. After identifying markers for all states within all samples

using the rank_genes_groups Scanpy command, we took the overlap of the markers from transcriptionally similar states across samples. Those markers that were present in two or more of the samples were then used to define gene State modules “A”, “B” and “C”.

A chi-squared test was used to determine the significance of association between cell cycle phase and state. Gene set enrichment analysis was then conducted with the Scanpy ‘score_genes’ command. The C6 oncogenic gene set collections from MSigDB were used for the gene set enrichment analysis.

Label transfer

scANVI, an extension of scVI, functions as an encoder to predict cell state labels given transcript abundances.[55] scANVI, an extension of scVI, was used as the classifier to transfer state labels between the samples. After taking in transcript abundances in the input layer, the model passes them through hidden layers and predicts the State label in the output layer. After training a reference model on one sample, we created a query model with the same weights and parameters from the reference model. The query models were then trained on a new sample and predicted state labels for those cells. The total loss for this model consisted of a combination of both the ELBO and classification loss. Cell type predictions were compared with known 'State' annotations by creating a contingency table, allowing assessment of the model's performance. From this contingency table, we could then compute F1 scores to assess precision and recall of these models.

RNA velocity and trajectory inference

Using scVelo, RNA velocity analysis was performed to identify trajectories within the OS PDX-derived cell lines[56]. scVelo, a recent RNA velocity tool, models transcription, splicing and degradation rates using the dynamical model.[57] RNA velocity models transcript kinetics to ultimately infer a cell’s state transition pattern, allowing for the inference of sources and terminal states within an embedding.

Transducing cells with lineage tracing construct

The lineage tracing construct used in this study was derived from the original perturb-seq vector which contained a barcode diversity of ~100,000[58] which contained 18-mer barcodes expressed on the 3’ UTR of BFP (pBA571). We generated lentiviral particles carrying the lineage tracing barcode library by transfecting HEK293T cells with pBA571. We subsequently transduced 3×10^6 cells of each cell line with these lentiviral particles. During this transduction process, the cells were cultured in DMEM + Glutamine with 5% BGS and a penicillin-streptomycin supplement. After the cells were infected at a low UMI (~7%) the BFP+ cells were sorted using the FACS Aria. The cells were then bottlenecked and expanded ~30 fold before being distributed into 18 wells to be treated with different drugs or with a DMSO control.

IC50 experiments

IC50 experiments for Cisplatin, an ATR 1895344 inhibitor and CDK 4/6 inhibitor were performed for all cell lines in a 96 well format in triplicates. Starting concentrations were 5 μM for Cisplatin, 0.5 μM for the ATR inhibitor, and 2 μM for the CDK4/6 inhibitor. Eight serial 1:3 dilutions were prepared for each drug in culture medium, with the highest DMSO concentration serving as the vehicle control. After quantifying viability with CellTiterGlo (Promega, G9241) and the BioTek Synergy neo2 plate

reader, the IC_{50} values were determined by fitting the data to a four-parameter logistic (4PL) model using the drm function from the 'drc' package in R.

FACS sorting

The cells used for the lineage tracing and Perturb-seq experiments were first spun down at 300g for 5 min and resuspended in cold PBS with 10% FBS. After the cells were passed through a 70*u*M filter and placed on ice, they were sorted for BFP and mCherry double positive signal using the BD FACS Aria and sorted into 50% DMEM medium and 50% FBS.

Treating the lineage tracing transduced cells and sequencing the barcodes from genomic DNA

The 15-day drug regimen included 3 days of treatment, a 3-day drug holiday and 7 more days of treatment. The 3-day drug holiday was included to allow resistant clones to proliferate.

Genomic DNA (gDNA) from the lineage tracing experiment was extracted using the DNeasy Blood and Tissue Kit (57205964, Qiagen). The barcodes were then amplified from the gDNA using Primer 1 and 2 for 25 cycles with an annealing temp of 71C with the KAPA HIFI master mix. The first PCR isolated the barcode from the gDNA and added on the Truseq read 1 and read 2 primer binding sequences. A second PCR was then performed to append the unique dual indices and P5 and P7 adapters to allow for Illumina sequencing. An annealing temp of 72C and 25 cycles was used for the second PCR. The barcodes were then assayed on the Agilent tape station and quantified on the Qubit 3.0 before being sequenced on the Illumina HiSeq or NovaSeq.

Primer 1: ACACTCTTTCCCTACACGACGCTCTTCCGATCTGCACAGTCGAGGCTGAT

Primer 2: GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTCAAACTGGGGCACAAGC

Lineage tracing barcode analysis

The whitelist for the lineage-tracing barcodes was created from the Day-0 control sample by plotting the ranked counts and designating a threshold close to the elbow to filter the dataset to 988 barcodes for OS384, 961 barcodes for OS742 and 1,216 barcodes for OS052. Additional barcode counts were added if the barcodes were within a hamming distance of one (hamming distance of one represents a difference of one base pair) from any barcode in the whitelist. We then filtered the barcode list in all the other conditions based on the whitelist and added values from non-whitelist barcodes that were within a hamming distance of one. To compare barcode representation in different conditions, we computed the log-fold change of the cpm scaled values between the treated samples and the day-13 control. The p-value for this analysis was computed using Pearson's chi-squared test with the assumption that the presence of one barcode does not influence the presence of another. The likelihood of lineage tracing barcode depletion based on the state was determined using a binary logistic regression model for each available combination of drug and cell line.

Trajectory driver identification

CellRank was used to infer terminal states and suspected lineage drivers.[59] The CellRank kernel employed in this study uses RNA velocity to infer directionality of the edges, representative of transition probabilities, within a markov chain. GPCCA, a CellRank estimator, was used to infer suspected drivers by correlating expression through pseudotime for each gene with absorption

probabilities for a given terminal state. These inferred drivers were filtered for p-values<0.05, correlations>0.2 and based on whether they were transcription factors.

A biologically informed VAE (MAVE) was also used to identify suspected regulators for the state “A” profile. The nodes within the first hidden layer of the MAVE model are representative of transcription factors. Larger weights between the first and second layer suggest a more active transcription factor within that batch of data. After feeding in a batch of data for cells within a certain state, one can compare how the nodes, representative of different transcription factors, have different weights which can be interpreted as variable activity in different transcriptomic states.

Perturb-seq experiment

The dual-guide vectors used for the Perturb-seq screen in this study were assembled with a 2-step method based on the protocol detailed in the Replogle manuscript.[30] First, ultramers containing two guide RNAs were designed for each of the 12 targets and cloned into pJR85 using Gibson cloning. These cloned constructs and pJR89 were then simultaneously digested, allowing for the tracr and promoter from pJR89, to be cloned into the intermediate construct using the Golden gate cloning method.

5’ Gibson overhang of ultramer: tgagactataagtatcccttggagaaccaccttgttgg
3’ Gibson overhang of ultramer: gtttaagagctaagctggaaacagcatagcaagtttaaataa

Example Ultramer Sequence:
tgagactataagtatcccttggagaaccaccttgttggggcaccgtgcctggcaccgcgtttcagagcgagacgtgcctgcaggatacgtctca
gaaacatggggatcgggagaagcgaagagtttaagagctaagctggaaacagcatagcaagtttaaataa

After generating viral particles for the dCas9-KRAB mCherry construct (Addgene 188779), cell lines were transduced and sorted based on mCherry expression.[31] The sorted cells were then transduced with constructs expressing dual guide RNAs for single targets and sorted for both BFP and mCherry expression. After culturing the cells for 3-5 days, the single cell libraries were then prepared with the 10X 3’ V3.1 kit.

Analyzing Perturb-seq dataset

Since the Perturb-seq transcript and gRNA libraries were submitted separately for sequencing, we received separate FASTQ files for each. This data was processed with cellranger with the –feature-ref and –libraries flag. We then associated the gRNA with the 10X cell barcode using the molecule_info.h5 object from the cellranger output.

We used a chi-squared analysis to test the statistical significance of cell proportions within different clusters in the context of different transcription factor knock-downs. In order to aggregate all of the samples into a single analysis, we also used a binary logistic regression model to predict the likelihood of cells being in State B given the transcription factor that was targeted for a certain cell and used the cell line as a covariate in the model.

Testing treatment efficacy improvements for single-target knockdowns

After generating virus for NFE2L3 and NR0B1 targets, the cell lines were transduced in 10 cm dishes and FACS sorted based on BFP and mCherry into 50% DMEM and 50% FBS. The cell lines were then plated in a 96-well format in triplicates and treated with the IC50 concentrations of Cisplatin, an ATR inhibitor, a CDK 4/6 inhibitor or DMSO for the same 15-day regimen as used for the lineage tracing experiment. We use the Cell Titer Glo (CTG) (Promega, G9241) viability assay to determine any efficacy improvements with the knockdowns. After the 15-day treatment, the cells were incubated with the CTG reagent for 30 min and the fluorescence was measured using the BioTek Synergy neo2 plate reader.

Code Availability: https://github.com/brendamelano/Reprogramming_Osteosarcoma

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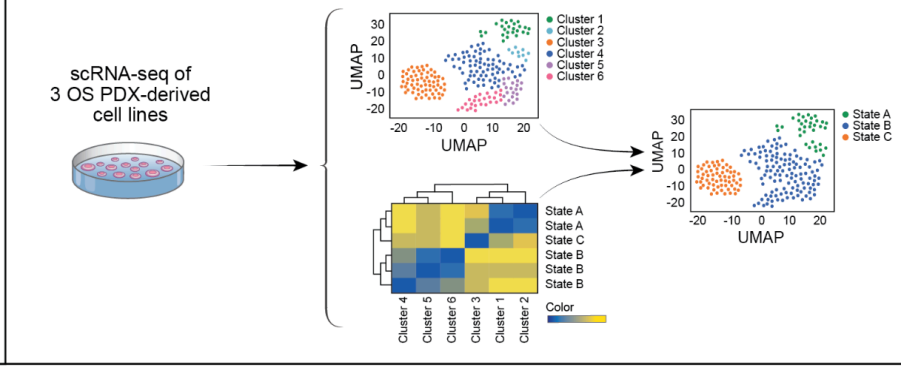
Figure 1

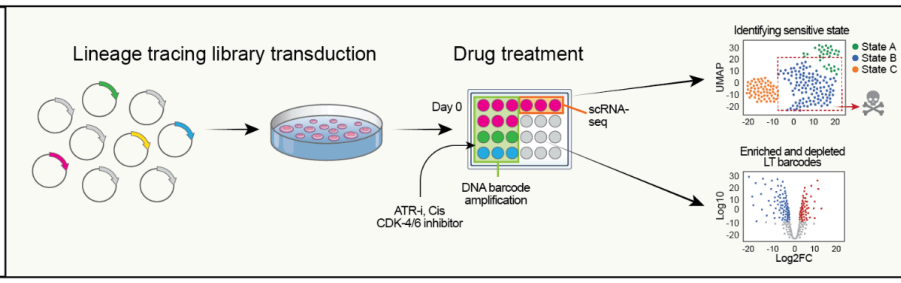
A

State characterization



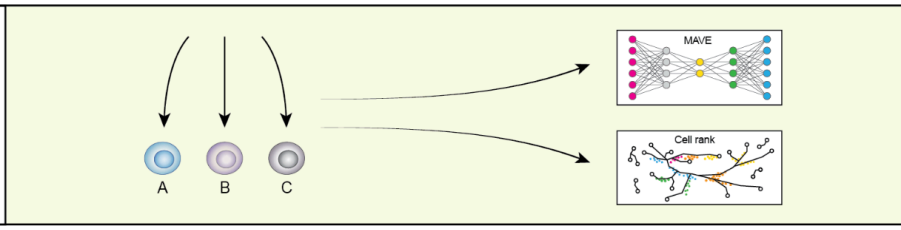
B

Identifying sensitive state



C

Driver identification



D

Reprogramming cells with Perturb-seq

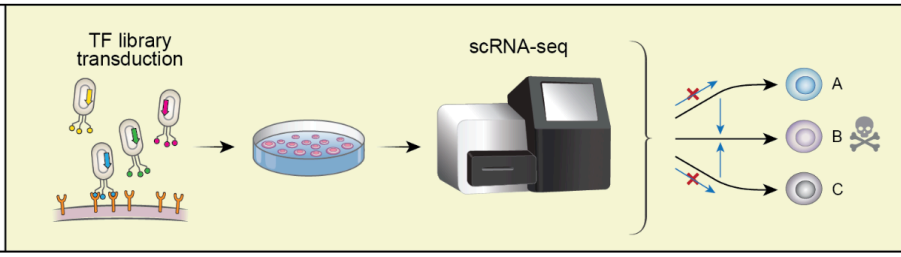


Figure 1: Schematic for target identification pipeline

(A) Single cell RNA sequencing on the OS PDX-derived cell lines allowed for the aggregation of clusters into three unique transcriptomic states.

(B) Lineage tracing constructs were transduced into the OS PDX-derived cell lines to test variable clonal sensitivity across various treatment conditions. After isolating the lineage tracing barcodes from both the genomic DNA and scRNAseq libraries, we could identify the sensitive state within the cell lines.

(C) Candidate State drivers were identified using CellRank and CiberATAC, which uses a biologically informed VAE to identify suspected regulators.

(D) The perturb-seq pipeline was used to identify which candidate TF regulators could successfully shift cells to the sensitive state.

Figure 2

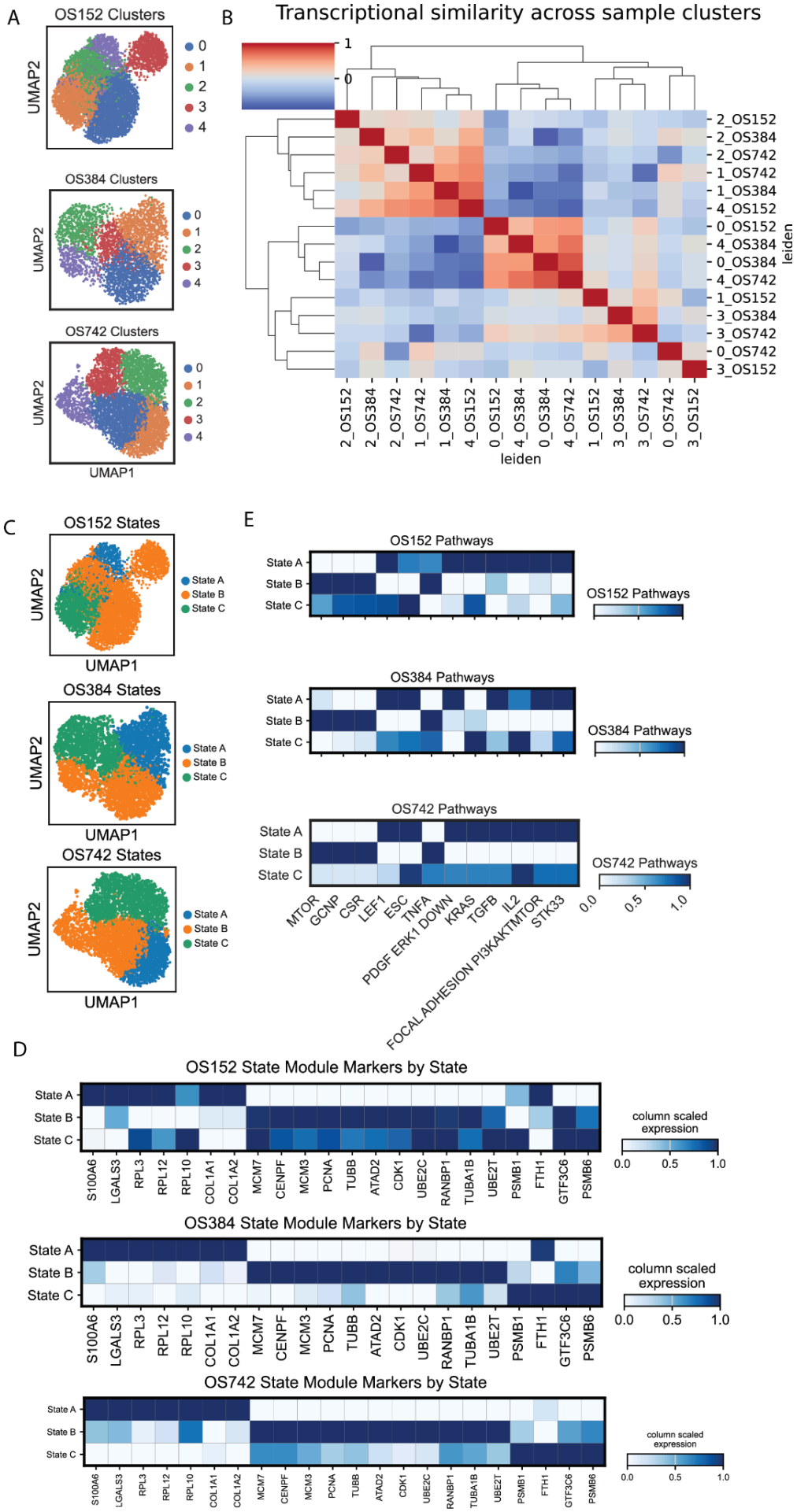

A
OS152 Clusters
OS384 Clusters
OS742 Clusters
UMAP2
UMAP1
0
1
2
3
4
B
Transcriptional similarity across sample clusters
1
0
2_OS152
2_OS384
2_OS742
1_OS742
1_OS384
4_OS152
0_OS152
4_OS384
0_OS384
4_OS742
1_OS152
3_OS384
3_OS742
0_OS742
3_OS152
leiden
C
OS152 States
OS384 States
OS742 States
State A
State B
State C
D
OS152 State Module Markers by State
OS384 State Module Markers by State
OS742 State Module Markers by State
S100A6
LGALS3
RPL3
RPL12
RPL10
COL1A1
COL1A2
MCM7
CENPF
MCM3
PCNA
TUBB
ATAD2
CDK1
UBE2C
RANBP1
TUBA1B
UBE2T
PSMB1
FTH1
GTF3C6
PSMB6
column scaled expression
0.0
0.5
1.0
E
OS152 Pathways
OS384 Pathways
OS742 Pathways
MTOR
GCNP
CSR
LEF1
ESC
TNFA
PDGF ERK1 DOWN
KRAS
TGFB
IL2
FOCAL ADHESION PI3KAKTMTOR
STK33

Figure 2: OS PDX-derived cell lines display transcriptomic intra-tumor heterogeneity and subtype classification.
(A) Uniform manifold approximation and projection (UMAP) of three OS patient derived xenograft (PDX)-derived cell lines: OS152, OS384 and OS742.
(B) Transcriptional similarity of clusters across different samples.
(C) Uniform manifold approximation and projection (UMAP) of three OS patient derived xenograft (PDX)-derived cell lines: OS152, OS384 and OS742. These plots show the State "A", "B" and "C" populations within these cell lines
(D) Matrix plot illustrating the expression of state module markers across OS152, OS384, and OS742 states. The gene markers are sorted by their state. This plot highlights the gene modules contributing to cellular states. The color bar represents column-scaled expression values.
(E) To confirm transcriptional similarity on the pathway level and identify which pathways are enriched in the different states, we quantified pathway enrichment in the different states. This analysis was performed on n=3 biological replicates.
(F) State module enrichment within the different states of OS152, OS384 and OS742.

Figure 3

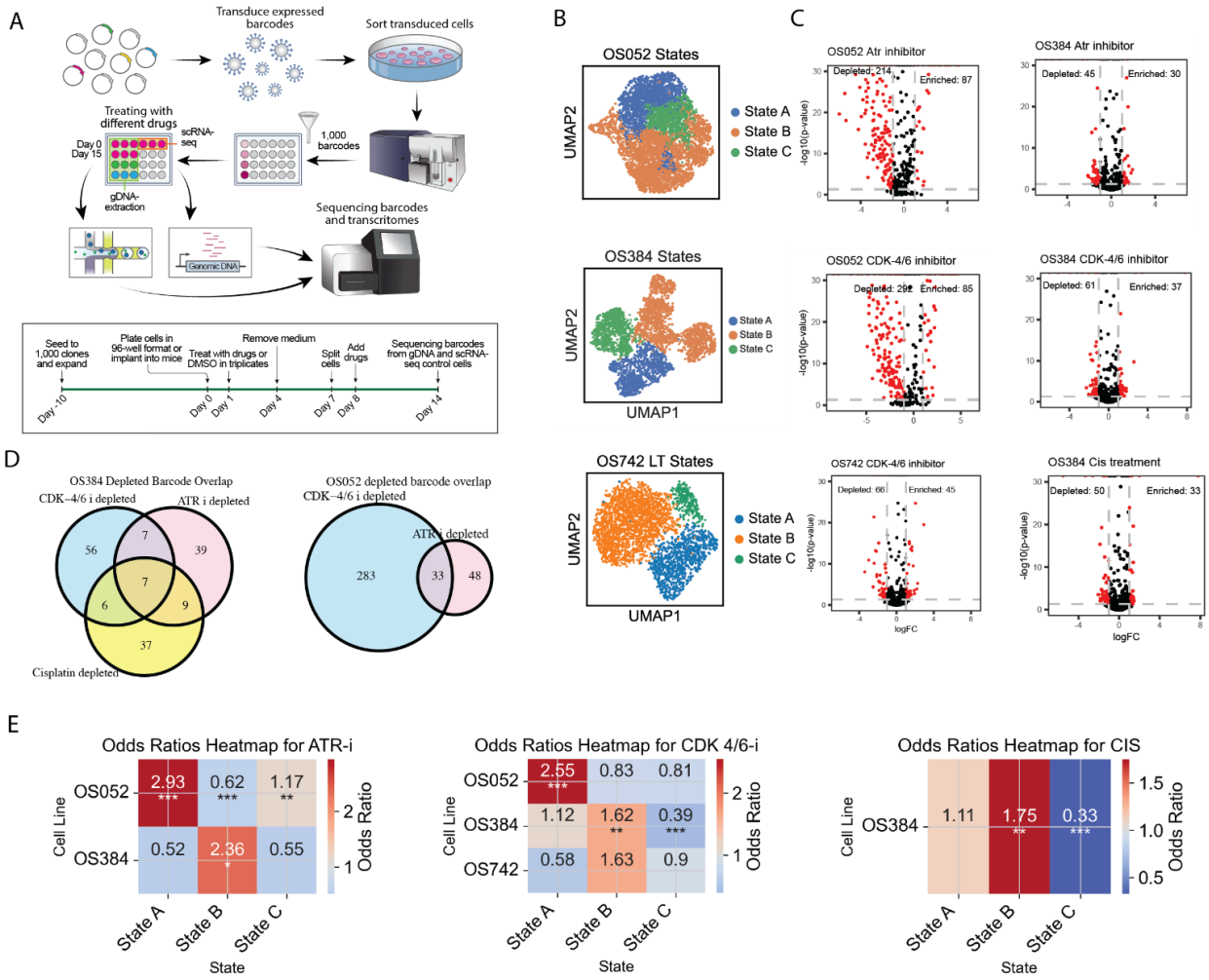

A
Transduce expressed barcodes
Sort transduced cells
Treating with different drugs
Day 0
Day 15
scRNA-seq
1,000 barcodes
gDNA-extraction
Sequencing barcodes and transcritomes
Genomic DNA
Seed to 1,000 clones and expand
Plate cells in 96-well format or implant into mice
Treat with drugs or DMSO in triplicates
Remove medium
Split cells
Add drugs
Sequencing barcodes from gDNA and scRNA-seq control cells
Day -10
Day 0
Day 1
Day 4
Day 7
Day 8
Day 14
B
OS052 States
UMAP2
UMAP1
State A
State B
State C
OS384 States
OS742 LT States
C
OS052 Atr inhibitor
Depleted: 214
Enriched: 87
OS384 Atr inhibitor
Depleted: 45
Enriched: 30
OS052 CDK-4/6 inhibitor
Depleted: 292
Enriched: 85
OS384 CDK-4/6 inhibitor
Depleted: 61
Enriched: 37
OS742 CDK-4/6 inhibitor
Depleted: 66
Enriched: 45
OS384 Cis treatment
Depleted: 50
Enriched: 33
-log10(p-value)
logFC
D
OS384 Depleted Barcode Overlap
CDK−4/6 i depleted
ATR i depleted
Cisplatin depleted
56
7
39
7
6
9
37
OS052 depleted barcode overlap
CDK−4/6 i depleted
ATR i depleted
283
33
48
E
Odds Ratios Heatmap for ATR-i
Cell Line
OS052
OS384
2.93 ***
0.62 ***
1.17 **
0.52
2.36 *
0.55
State A
State B
State C
State
Odds Ratio
Odds Ratios Heatmap for CDK 4/6-i
OS052
OS384
OS742
2.55 ***
0.83
0.81
1.12
1.62 **
0.39 ***
0.58
1.63
0.9
Odds Ratios Heatmap for CIS
OS384
1.11
1.75 **
0.33 ***

Figure 3: Identifying the sensitive state using lineage tracing.

(A) Experimental pipeline for the lineage tracing approach to identify the sensitive state in the OS PDX-derived cell lines. Here, we transduced cells with lentiviral particles containing the expressed barcodes and sorted the transduced cells using blue fluorescent protein (BFP). The cells were then bottlenecked to 1,000 cells and expanded prior to being treated with different drugs. Every treatment condition in the experiment was performed on n=3 technical replicates. After treatment with a 15-day drug regimen, the amplified barcodes and single-cell libraries were sequenced.

(B) Here, we are showing the scRNA-seq clustered embeddings for the untreated OS052, OS384 and OS742 cell lines after being transduced with the lineage tracing barcode library. The cells that were sequenced for this experiment included cells from n=3 technical replicates for untreated controls.

(C) Enriched and depleted lineage tracing barcodes in OS052. The enriched and depleted barcodes for the ATR inhibitor, a CDK 4/6 inhibitor and Cisplatin in OS052 are highlighted in red and were defined as those that had p-values less than 0.05 and log_2 fold-change less than 1 (for depleted barcodes) or more than 1 (for enriched barcodes)

(D) Enriched and depleted lineage tracing barcodes in OS384. The enriched and depleted barcodes for the ATR inhibitor, a CDK 4/6 inhibitor and Cisplatin in OS384 are highlighted in red and were defined as those that had p-values less than 0.05 and log_2 fold-change less than 1 (for depleted barcodes) or more than 1 (for enriched barcodes)

(E) To determine the likelihood of lineage tracing barcodes being depleted based on the State the cell was in, we performed a binary logistic regression. We are showing a heatmap of the odds ratio for each state and available cell lines.

(F) The venn diagrams illustrate the overlap of depleted barcodes in OS384 treated with CDK-4/6 inhibitor (CDK-4/6 i), ATR inhibitor (ATR i), and Cisplatin and the overlap of depleted barcodes in OS052 with CDK 4/6 and ATR inhibitors. The overlap between each pair of depleted barcode sets is shown. Fisher's Exact Test was used to evaluate the significance of the barcode overlaps with pairwise comparisons and adjusted p-values with Benjamini-Hochberg (CDK 4-6 i vs. ATR i p=0.000431, ATR i vs. Cis p=1.16e-06 and CDK 4/6 i vs. Cis p = 0.000662). A hypergeometric test was also performed to determine the significance of the 3-way overlap (p=0.25).

Figure 4

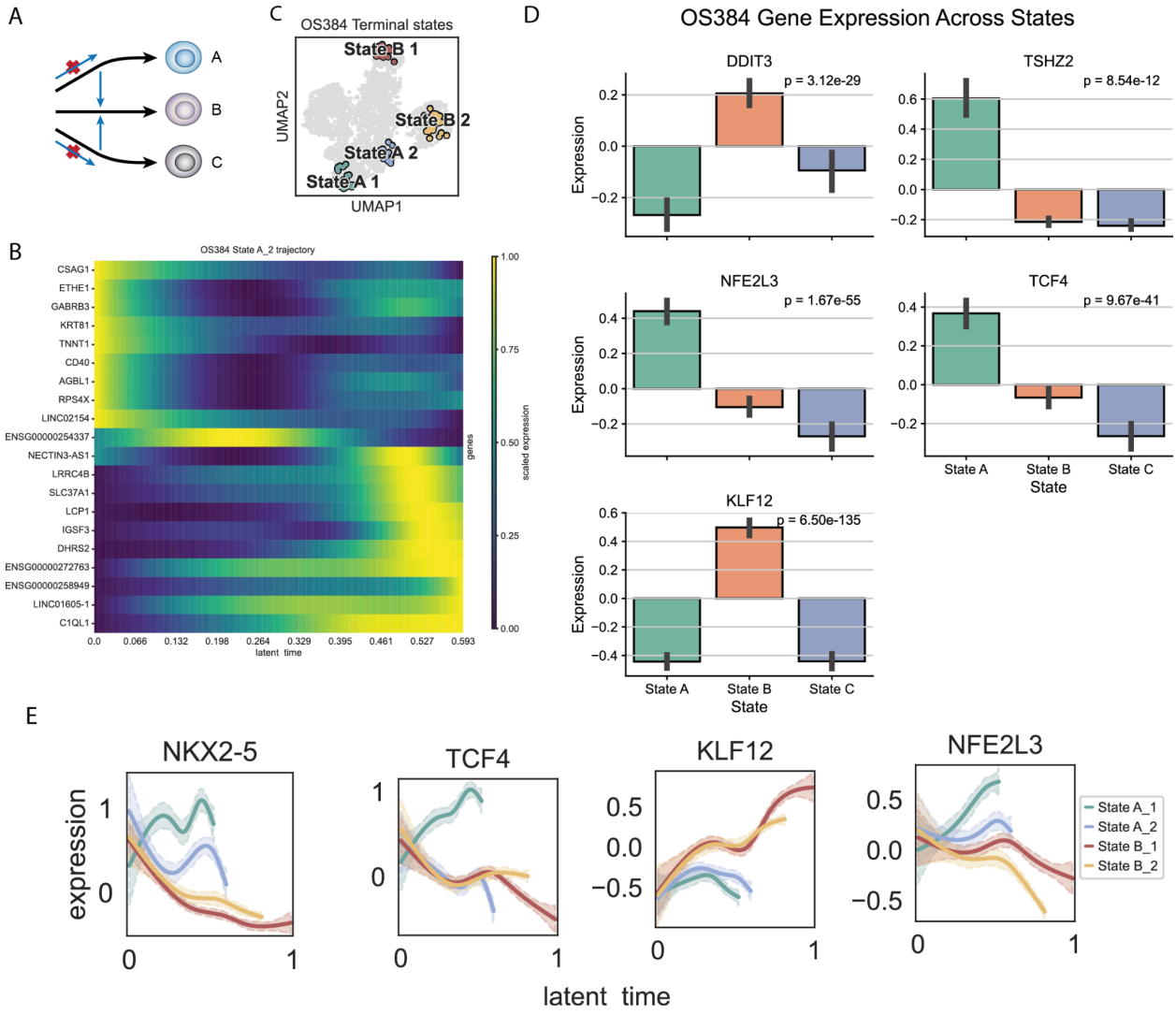


Figure 4: Identifying OS PDX-derived cell lineage drivers using CellRank and a biologically informed Variational Autoencoder (VAE)

(A) The goal of this analysis is to identify lineage drivers that can reprogram cells from resistant states to those associated with more sensitive phenotypes. By identifying these critical transcription factors (TFs), we aim to modulate entire cellular states to enhance sensitivity in OS PDX-derived cell lines.

(B) Here, we show the terminal macrostates of the OS384 cell line as predicted by CellRank using the "top_n" method with four states selected. The UMAP embedding visualizes these terminal states within their associated clusters. Each distinct color represents a different terminal state.

(C) The bar plots display the mean expression levels of the identified lineage drivers across distinct transcriptional states identified in the OS384 lineage-tracing dataset. Each bar shows the mean expression for a given state with error bars indicating the standard deviation (SD). Corrected p-values are calculated using Kruskal-Wallis tests followed by Benjamini-Hochberg correction for multiple testing, with a significance threshold of 0.05.

(D) The heatmap shows the expression of the top 20 driver genes associated with the "State A_2" terminal state in OS384. Cells are ordered along the x-axis based on pseudotime progression, while rows represent driver genes identified for the selected lineage. Color intensity reflects gene expression levels, with brighter colors indicating higher expression.

(E) To confirm variable expression of the CellRank identified lineage drivers, we quantified expression of the TFs through pseudotime for the four terminal states identified by CellRank. Here, we show the expression of *NFE2L3*, *TCF4* and *NKX2-5* through pseudotime in the OS384 LT transduced cell line.

Figure 5

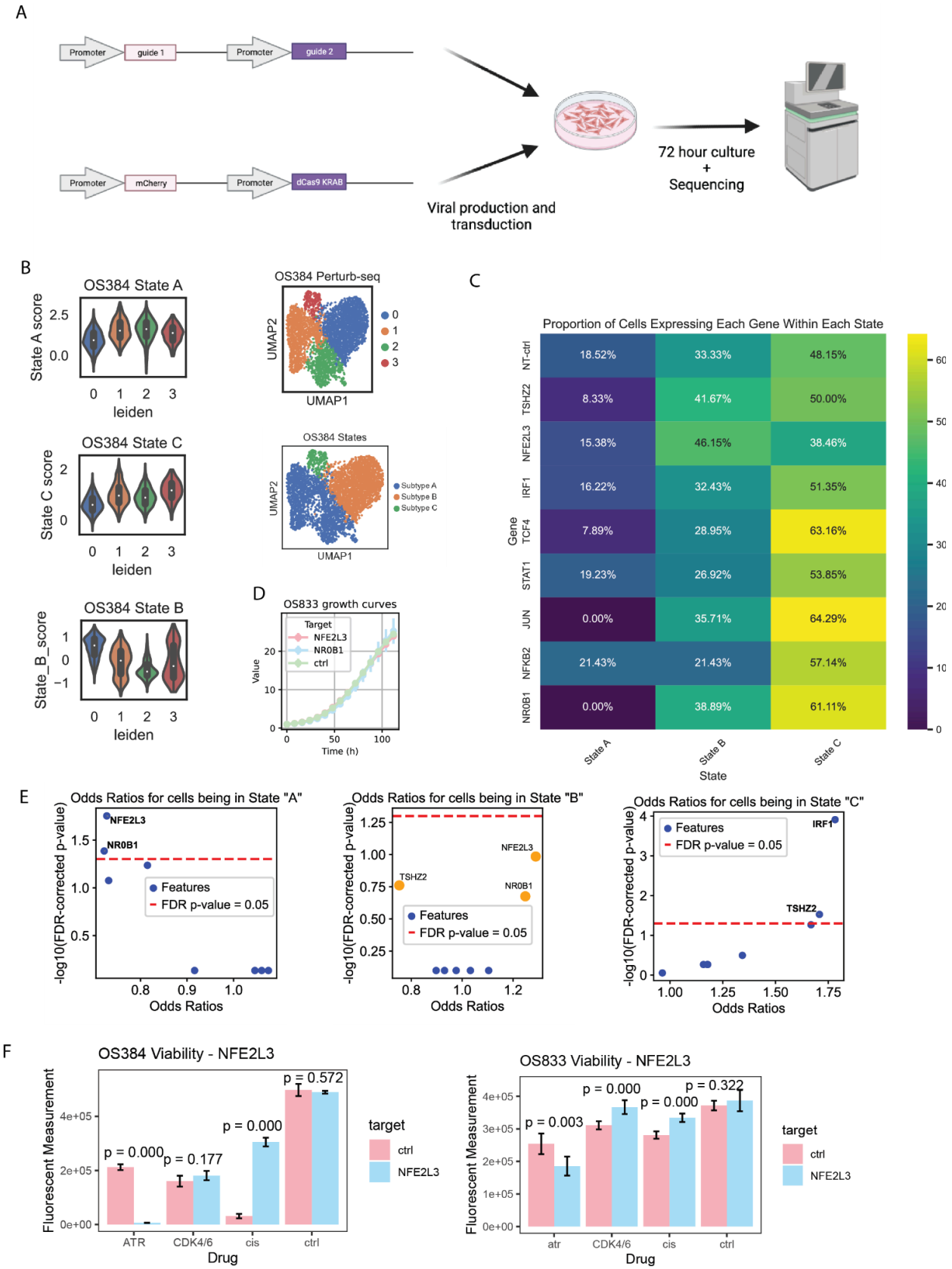


Figure 5: Using Perturb-seq to test reprogramming capabilities and testing efficacy improvements after perturbations. **(A)** Experimental pipeline for the Perturb-seq experiment. After generating three OS-PDX derived cell lines co-expressing mCherry and dCas9-KRAB (CRISPRi), we transduced the OS PDX-derived cell lines with lentiviral particles containing

constructs with dual-guide RNAs for the same target in addition to BFP. The cells were then sorted for double positive mCherry and BFP and processed with the 10X 3' v3.1 kit

(B) GEO: X was used to generate the perturb-seq embedding for OS384. These cells were transduced with the perturb-seq library. On the right, we are showing enrichment of the State B module in the different clusters identified using the Leiden cluster algorithm.

(C) The heatmap shows the percentage of cells within each state based on the TF targeted within that cell, with NT-ctrl as a non-targeting control. Each cell is annotated with the percentage of cells within each state, and the color intensity reflects these values.

(D) To determine whether the knockdown of ant of the TFs in the perturb-seq library increased the likelihood of cells being in State "B" and to combine OS384, OS742 and OS833 — the cell lines used in the perturb-seq experiment —, we performed a multinomial regression analysis. Here we are showing the log odds ratio for the different TFs with a p value cutoff of 0.05.

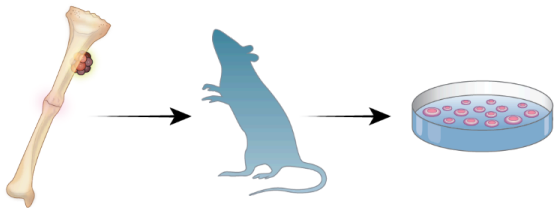
(E) We compared NFE2L3 and NR0B1 knockdown cell lines and control cell lines by plating the cells with n=6 technical replicates in a 96 well format and quantifying confluency with the incucyte. The control cell line is highlighted in green while the NFE2L3 and NR0B1 knockdown cell lines are highlighted in red and green respectively. The error bars represent standard deviations for the technical replicates.

(F) To test sensitivity differences to an ATR inhibitor after knockdown of NFE2L3, we treated the control and NFE2L3-KD cells with the 15 day drug regimen and quantified viability with the CellTiter Glo assay. Error bars represent standard deviations for the n=3 technical replicates and the p values were computed using a Student's t-test.

Supplemental Figures

Supplemental 1

A



Sample	Amplification	Source
OS152	MYC	Metastatic
OS384	VEGFA	Resection
OS742	MYC and CDK4	Diagnostic

B

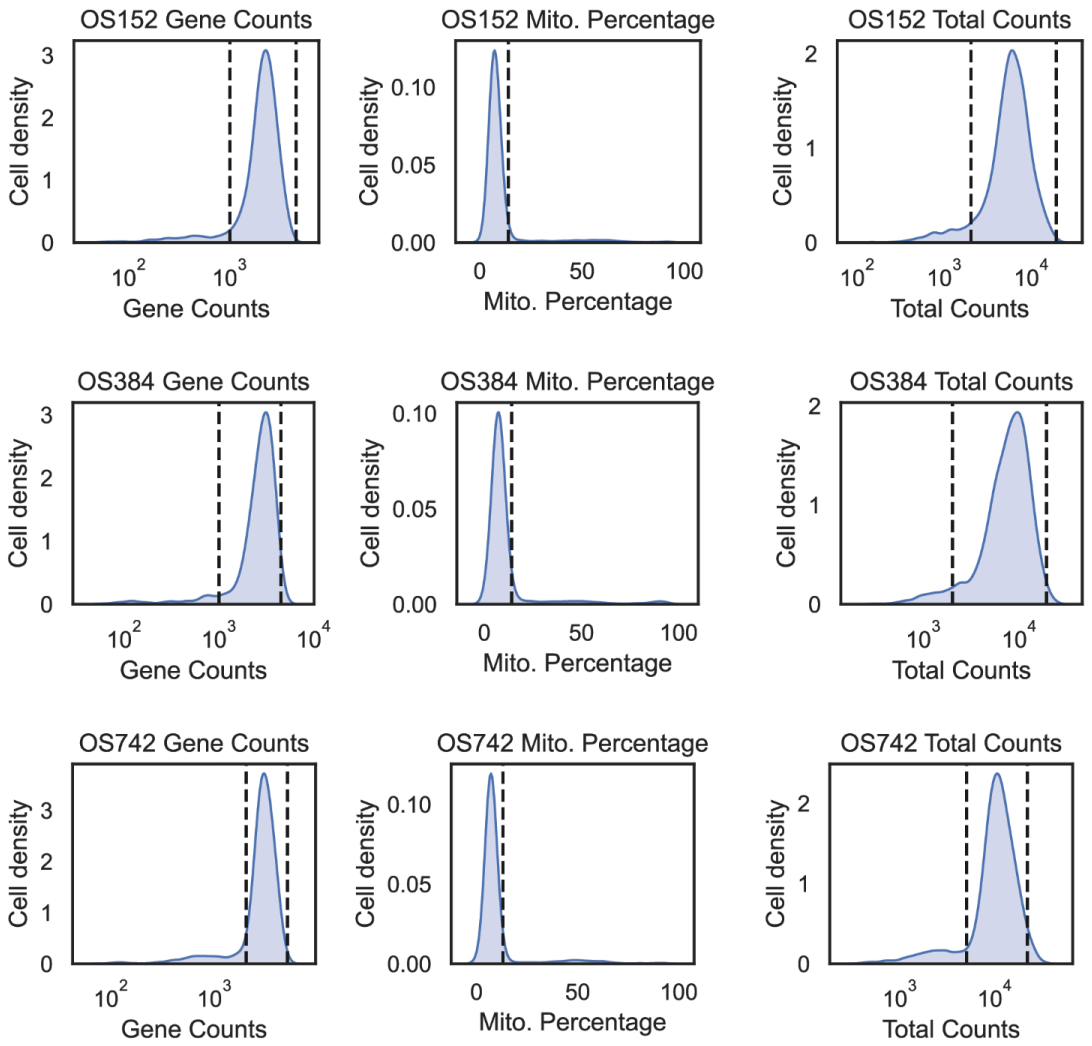
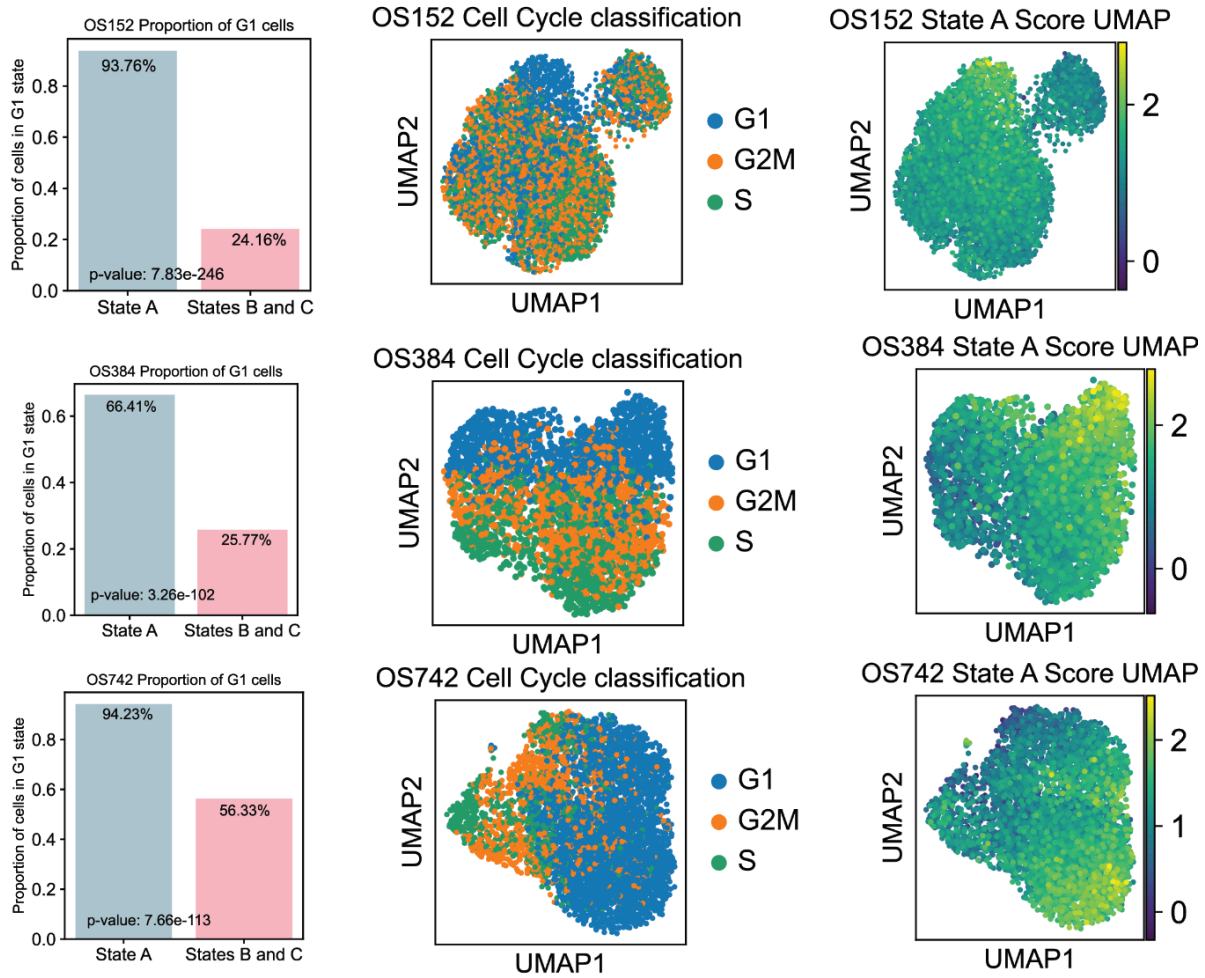


Figure S1: Sample descriptions and quality control analysis for scRNA-seq of OS PDX-derived cell lines.
(A) Overview of three osteosarcoma (OS) PDX-derived cell lines—OS152, OS384, and OS742—each exhibiting amplifications in MYC, VEGFA, and CDK4. These cell lines originated from different sources and were selected for single-cell RNA-sequencing (scRNA-seq) analysis.

(B) Quality control filtering applied to the scRNA-seq datasets, based on total read counts, number of detected genes per cell, and mitochondrial gene expression percentages.

Supplemental 2:

A



B

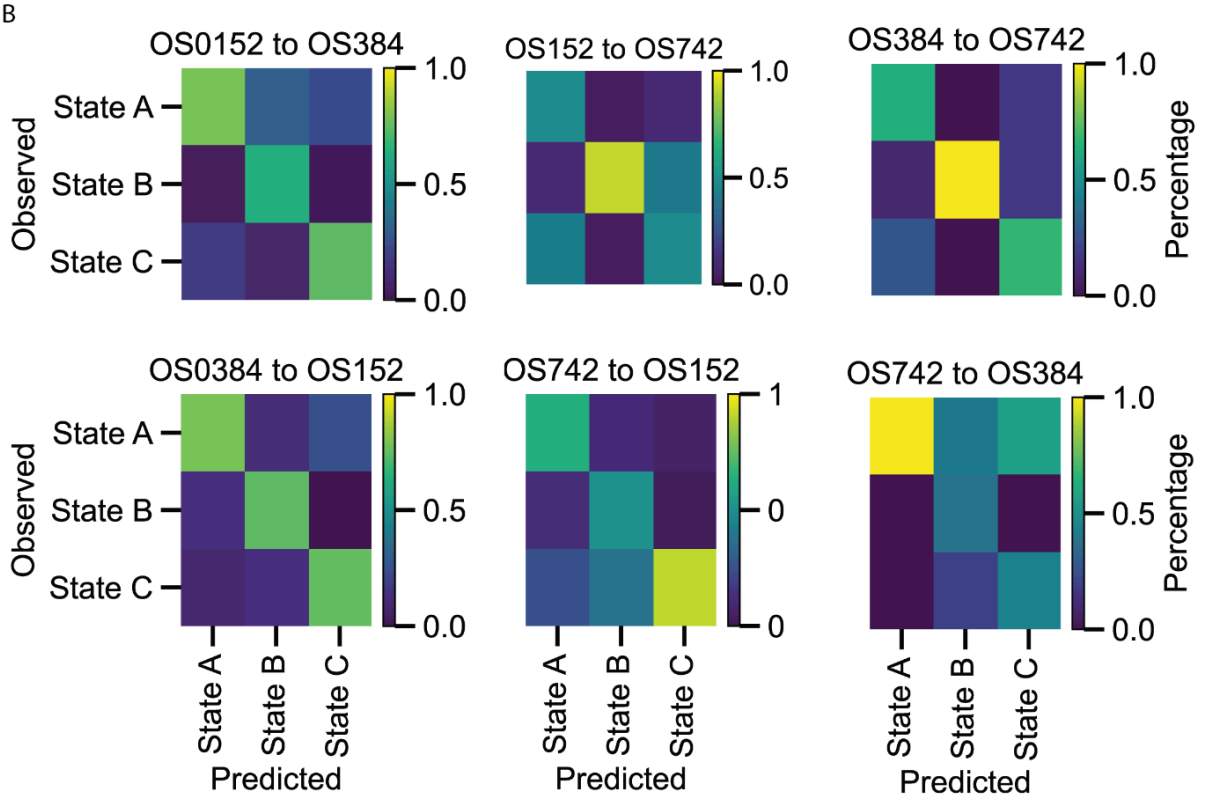
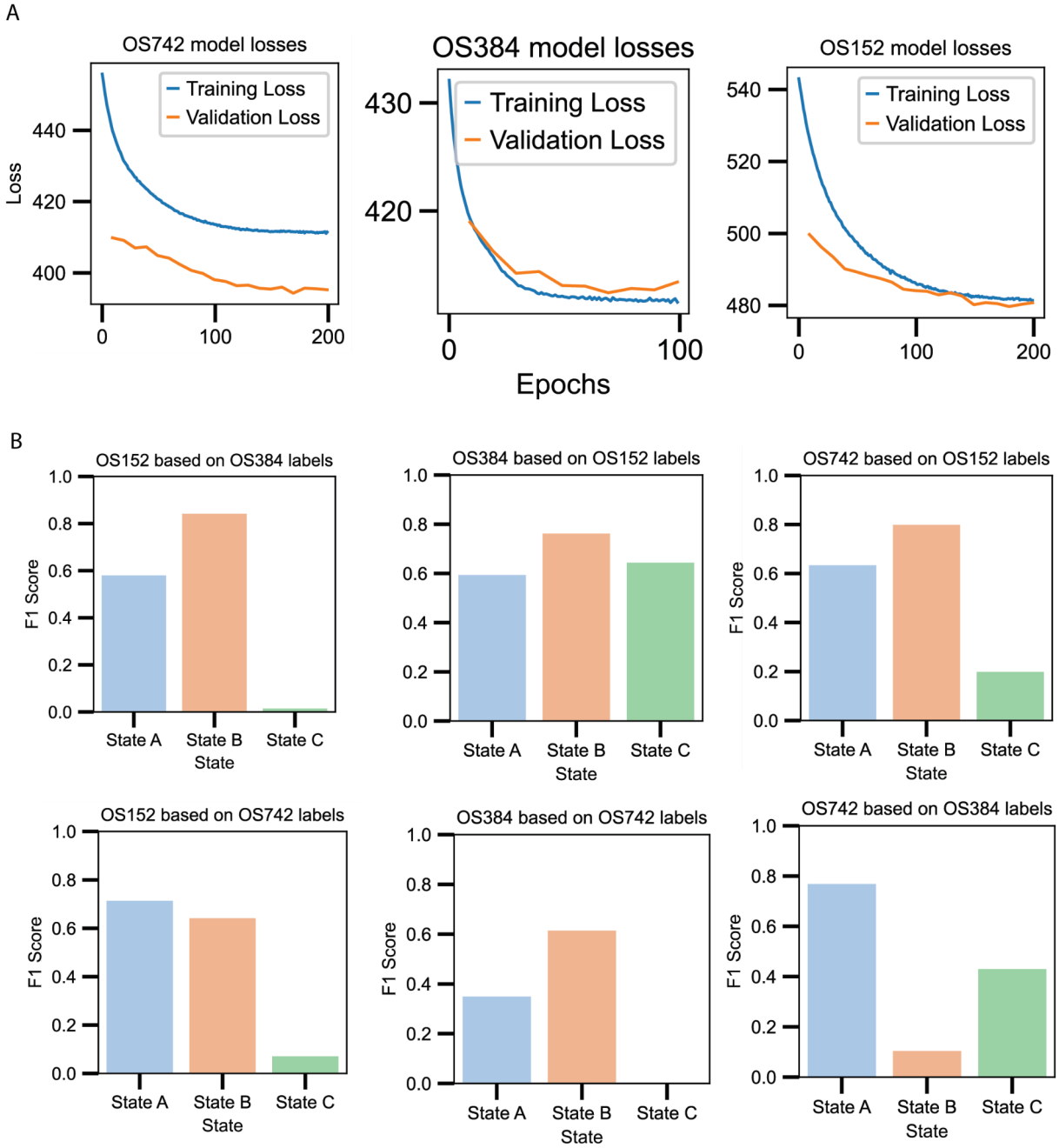


Figure S2: Demonstrating sample level transcriptional similarities with State gene module marker enrichment and a label transferring method

(A) OS152, OS384 and OS742 UMAP embeddings colored for cell cycle phase and State A module enrichment score. A chi-squared test was used to determine the significant association between the G1 phase and the State "A" population. **(B)** scANVI models were trained on the first sample in each subplot title and tested on the second sample. The vertical axis represents the State labels defined by enriched pathways and markers while the horizontal axis represents subtype labels as predicted by the scANVI models.

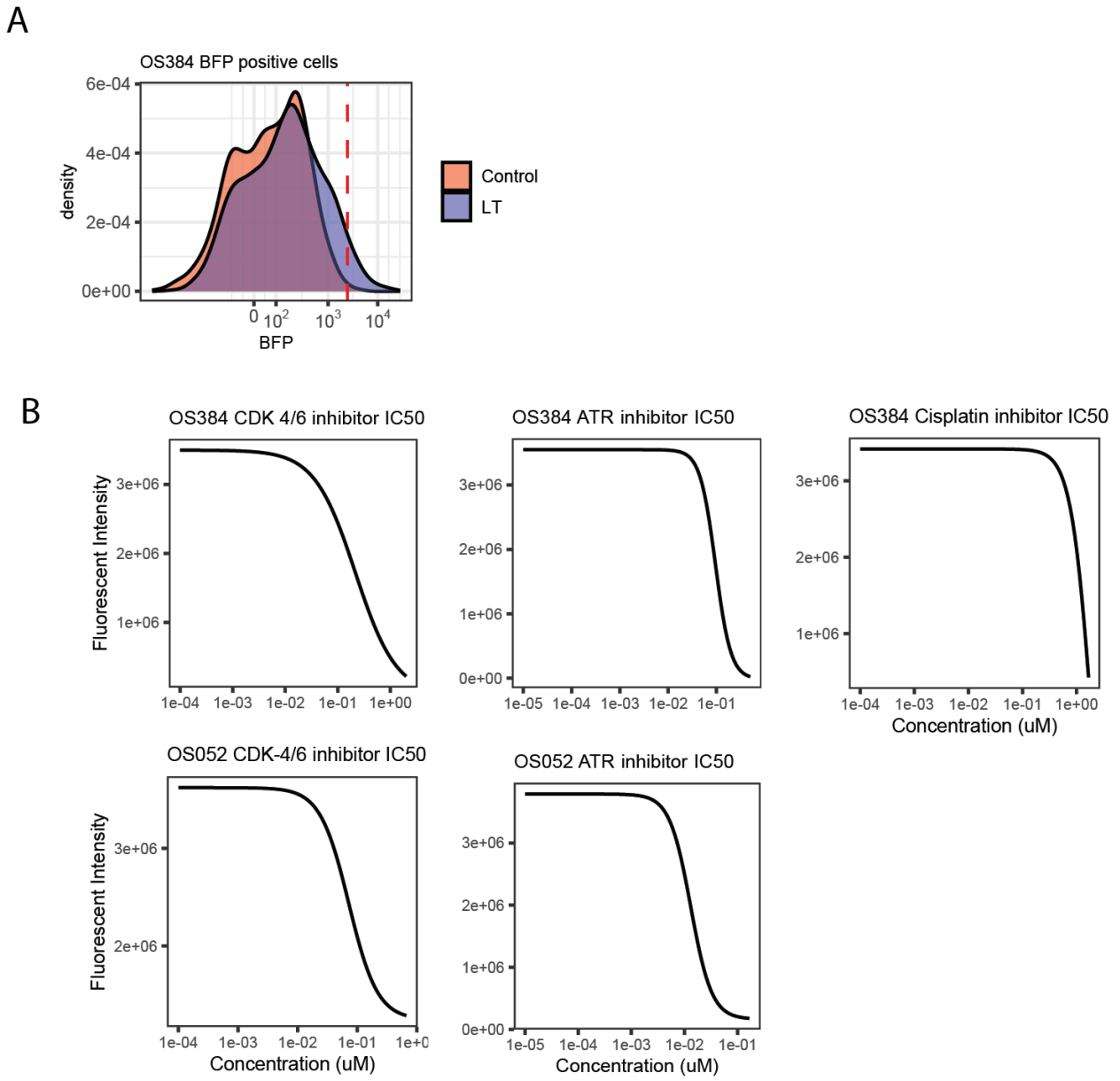
Supplemental 3



Supplemental 3: Accuracy and precision for state prediction in different samples.

A) The plots show the ELBO (Evidence Lower Bound) loss over epochs for both the training (blue line) and validation (orange line) datasets. The convergence of the loss curves and the minimal gap between them indicate successful model training with minimal overfitting.
B) The bar plots show F1 scores for each transcriptional state, comparing predicted labels to true labels for all possible training and prediction combinations between OS152, OS384 and OS742. These scores reflect the harmonic mean between precision and recall.

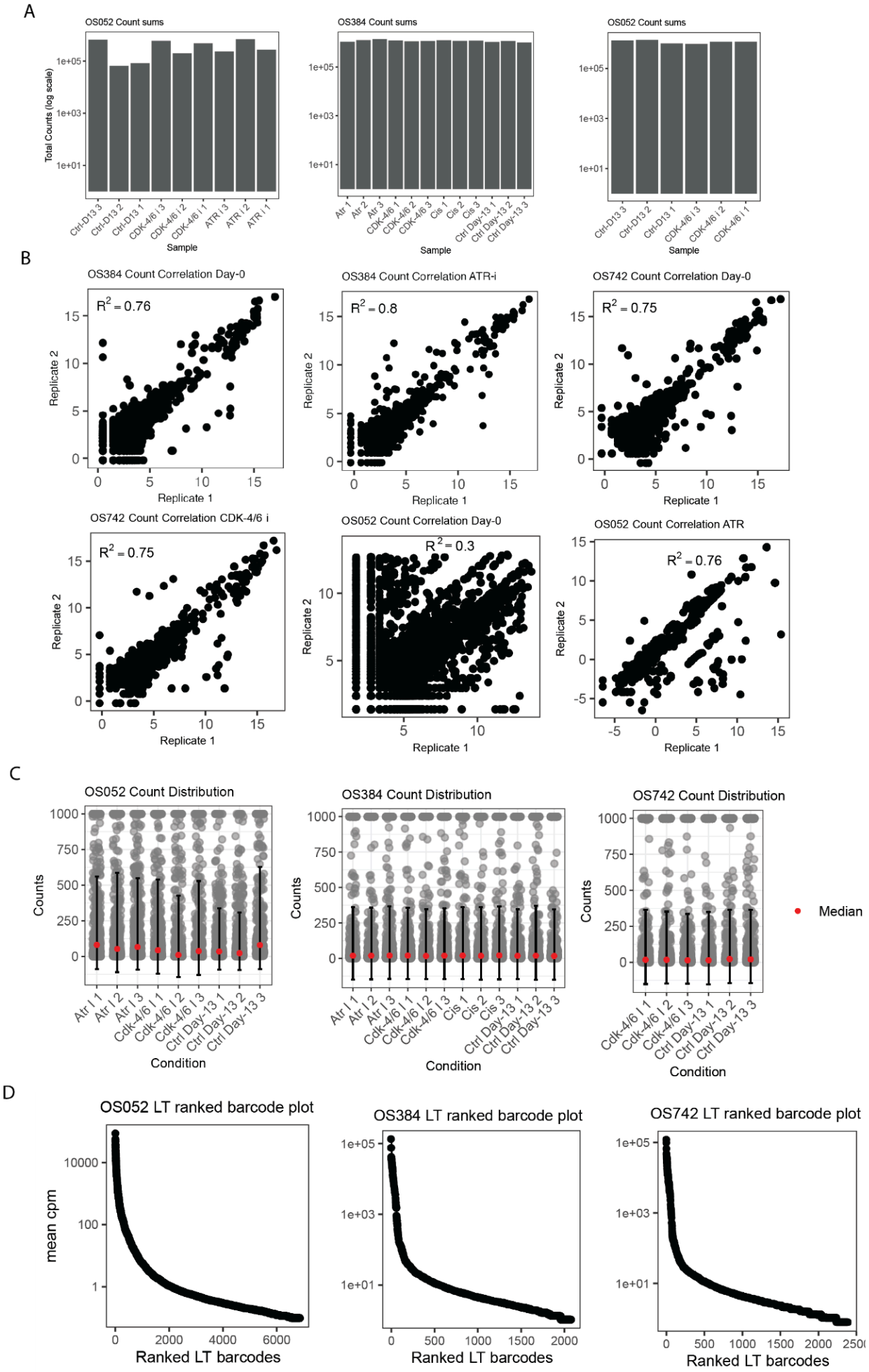
Supplemental 4



Supplementary Figure 4: Lineage tracing sort and dose-response analysis for 15 day drug regimen used for the Lineage tracing experiment
(A) The overlapping histogram plots represent the BFP intensity for OS384 wild-type and lineage tracing transduced cells. Lineage tracing transduced OS384 cells are represented with the blue curve while the control cells are represented by the red curve.

(B) The IC50 values for all drugs used on OS384 cells were determined using a dose-response assay. Cell viability was measured at varying concentrations over a 15-day period, and data were collected in triplicate. The data were fit using a four-parameter logistic regression model (LL.4), with the Hill slope, minimum, maximum, and EC50 as parameters. Fluorescent intensity was used as a proxy for cell viability. The x-axis is presented on a logarithmic scale to better visualize the concentration range.

Supplemental 5


A
OS052 Count sums
Total Counts (log scale)
1e+05
1e+03
1e+01
Ctrl-D13 3
Ctrl-D13 2
Ctrl-D13 1
CDK-4/6 I 3
CDK-4/6 I 2
CDK-4/6 I 1
ATR I 3
ATR I 2
ATR I 1
Sample
OS384 Count sums
Atr 1
Atr 2
Atr 3
CDK-4/6 1
CDK-4/6 2
CDK-4/6 3
Cis 1
Cis 2
Cis 3
Ctrl Day-13 1
Ctrl Day-13 2
Ctrl Day-13 3
Sample
OS052 Count sums
Sample
B
OS384 Count Correlation Day-0
$R^2 = 0.76$
OS384 Count Correlation ATR-i
$R^2 = 0.8$
OS742 Count Correlation Day-0
$R^2 = 0.75$
OS742 Count Correlation CDK-4/6 i
$R^2 = 0.75$
OS052 Count Correlation Day-0
$R^2 = 0.3$
OS052 Count Correlation ATR
$R^2 = 0.76$
Replicate 1
Replicate 2
C
OS052 Count Distribution
OS384 Count Distribution
OS742 Count Distribution
Counts
Condition
Median
D
OS052 LT ranked barcode plot
OS384 LT ranked barcode plot
OS742 LT ranked barcode plot
mean cpm
Ranked LT barcodes

Supplementary Figure 5: Lineage tracing sort and QC for barcodes amplified from gDNA

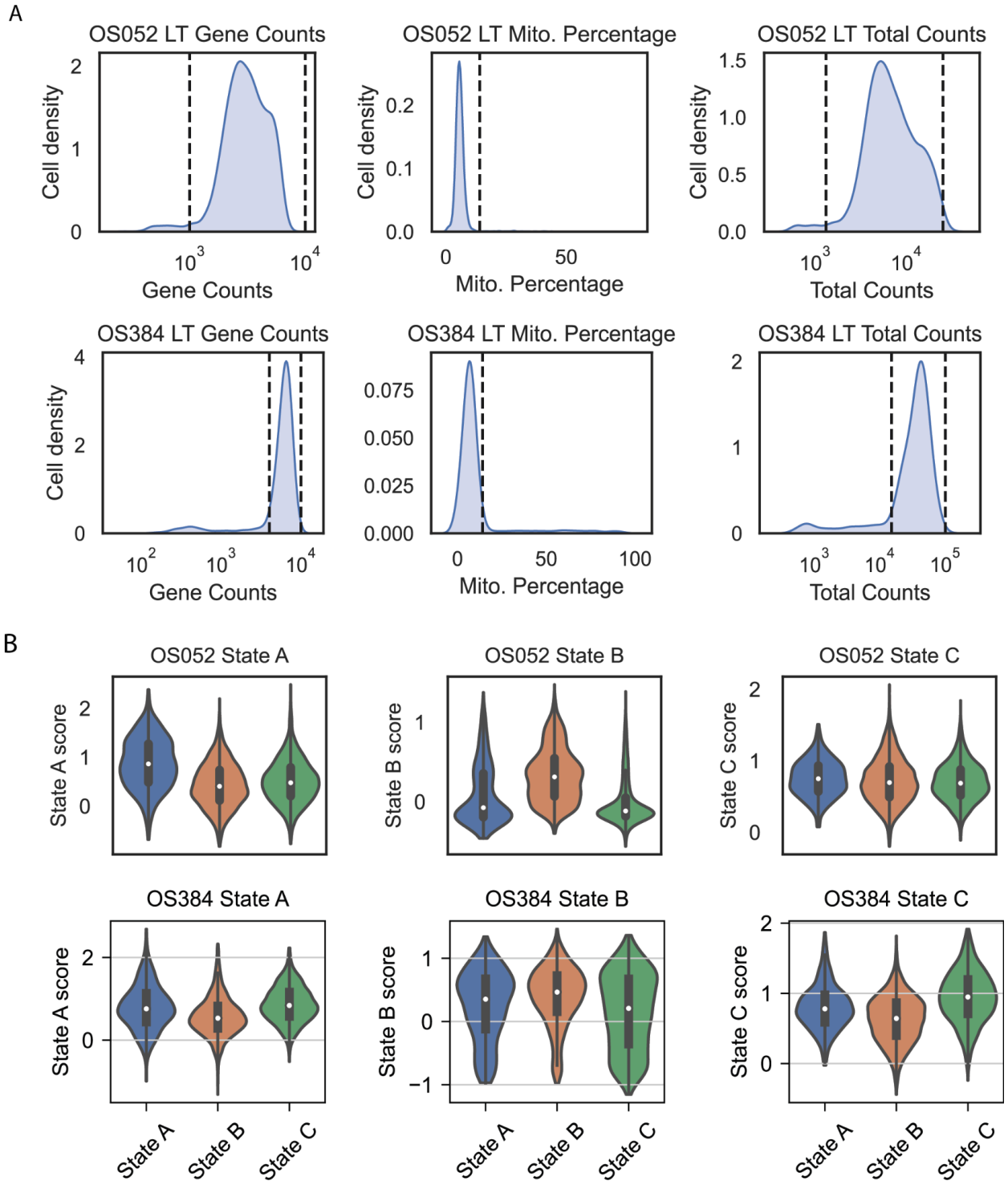
(A) Total raw counts for all replicates within OS052 and OS384 after filtering on whitelist generated from the Day-0 samples.

(B) Linear regression was used to compute the R^2 for the correlation between the technical replicates for the cpm-scaled and log-transformed barcode counts.

(C) Here, we plot the distribution of barcode counts across various conditions for OS052 and OS384, with individual data points (gray), median values (red), and error bars representing the mean ± standard deviation. Counts were capped at 1,000 to reduce the influence of extreme outliers, and x-axis labels were adjusted for clarity. Conditions include "Ctrl Day-13", "CDK-4/6 i", and "Atr i".

(D) The plots depict the ranked abundance of lineage-traced (LT) barcodes based on the mean CPM (counts per million) values for each barcode in each osteosarcomaPDX-derived cell-line. The x-axis represents the ranked LT barcodes, while the y-axis shows the mean CPM values on a logarithmic scale.

Supplemental 6

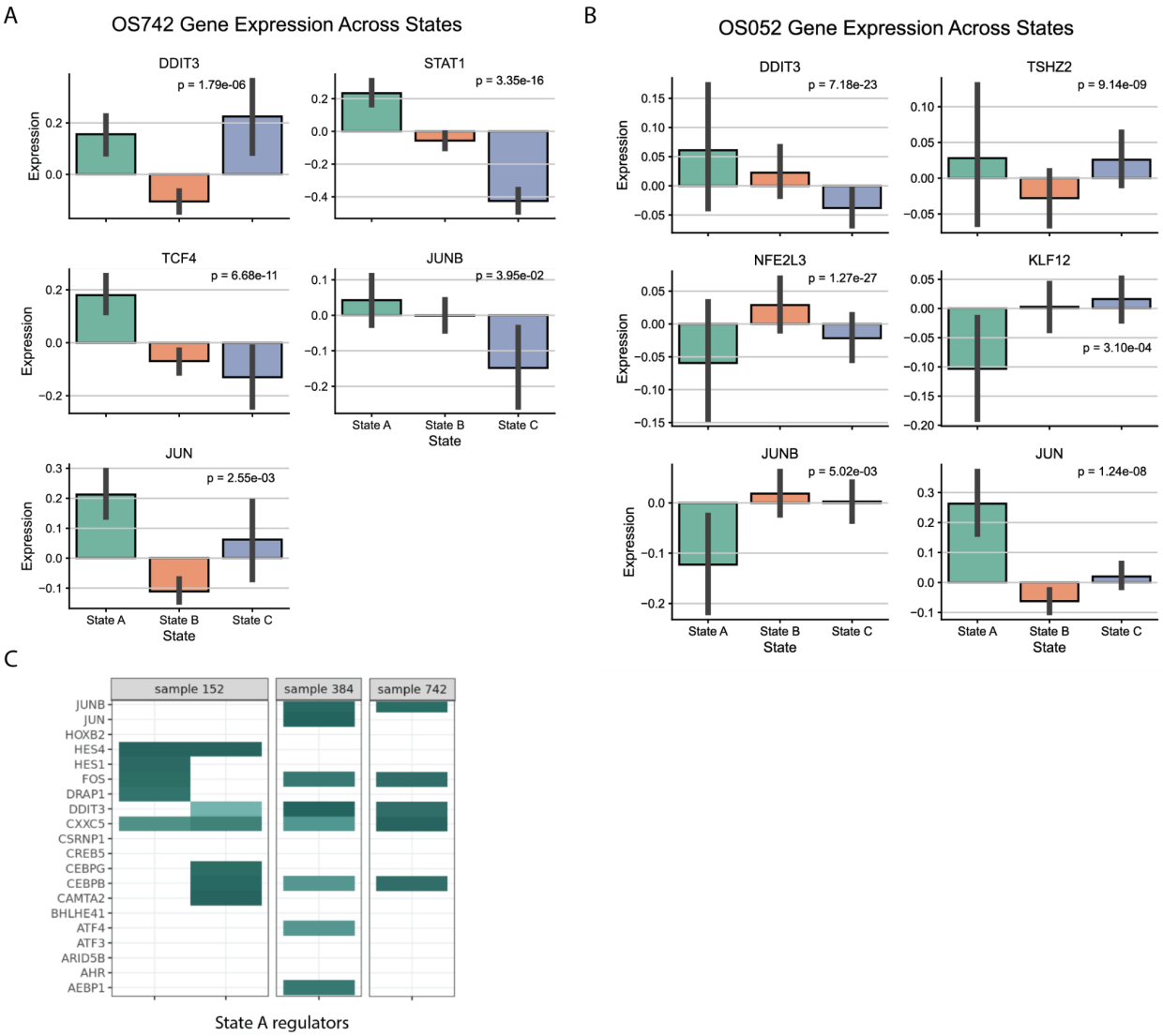


Supplementary Figure 6: scRNAseq QC for lineage tracing experiment

(A) The plots show the distribution of quality control metrics for the OS052 and OS384 samples, including the number of detected genes (Gene Counts), mitochondrial gene expression percentage (Mito. Percentage), and total RNA counts per cell. Vertical dashed lines indicate threshold values used to filter out cells based on each metric.

(B) State module enrichment in different States for the OS384 and OS052 lineage tracing transduced PDX-derived cell line.

Supplemental 7



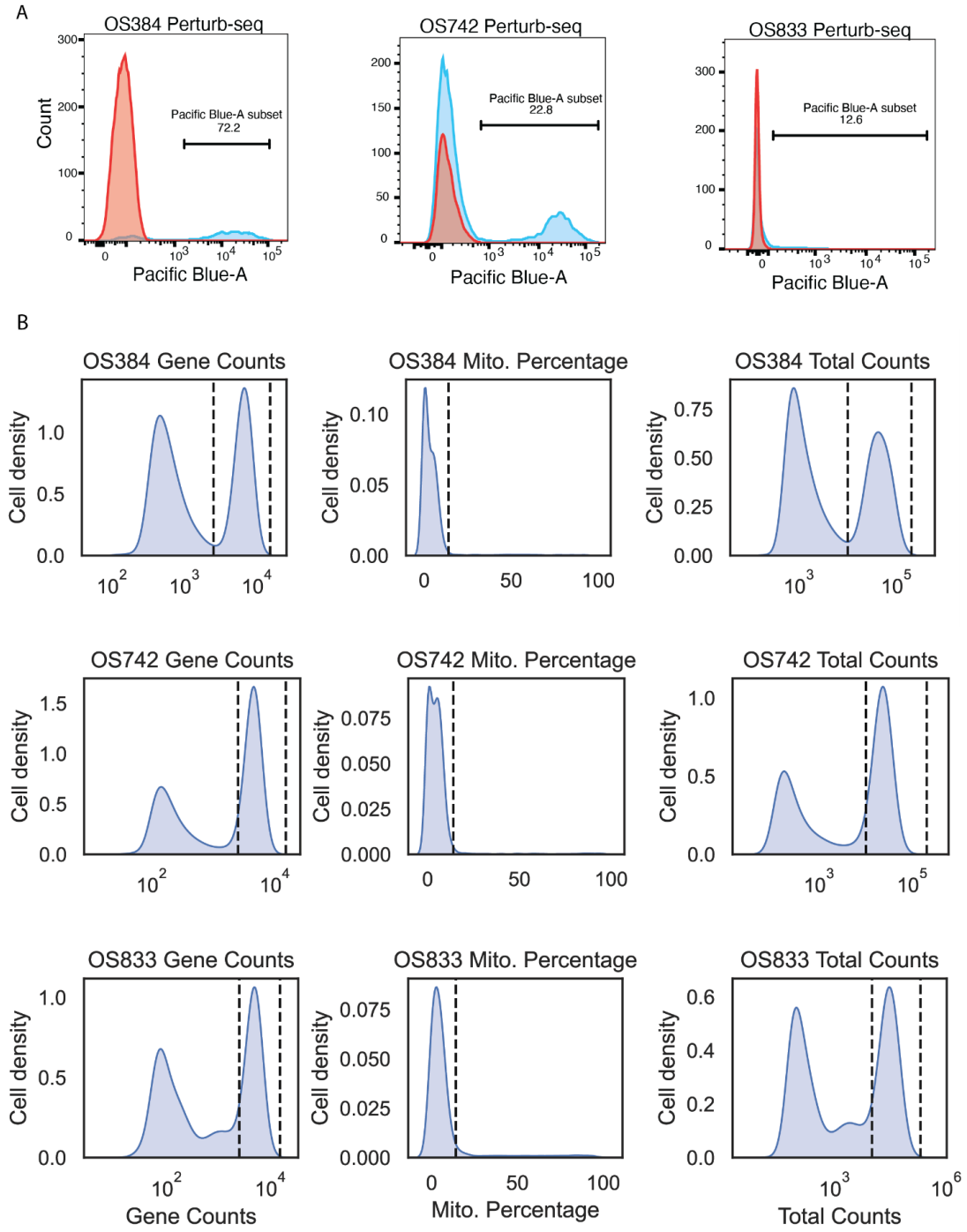
Supplementary Figure 7: Identifying suspected drivers for States "A"

(A) The expression levels of selected genes were quantified and visualized across different transcriptional states in OS742 using a bar plot for each gene. Each panel corresponds to an individual gene (e.g., *DDIT3*, *STAT1*, *NR0B1*, etc.), and the x-axis represents the States "A", "B" and "C". Bars show the mean expression levels with standard error bars. Statistical significance between states was assessed using the Kruskal-Wallis test, and p-values were corrected for multiple testing using the Benjamini-Hochberg (BH) method. The corrected p-values are indicated in each panel.

(B) The expression levels of selected genes were quantified and visualized across different transcriptional states in OS052 using a bar plot for each gene. Each panel corresponds to an individual gene (e.g., *DDIT3*, *STAT1*, *NR0B1*, etc.), and the x-axis represents the States "A", "B" and "C". Bars show the mean expression levels with standard error bars. Statistical significance between states was assessed using the Kruskal-Wallis test, and p-values were corrected for multiple testing using the Benjamini-Hochberg (BH) method. The corrected p-values are indicated in each panel.

(C) State "A" regulating transcription factors were identified by MAVE, a biologically informed VAE. We are showing MAVE transcription factor weights for OS152, OS384, and OS742 after incorporating in bulk ATAC data.

Supplemental 8

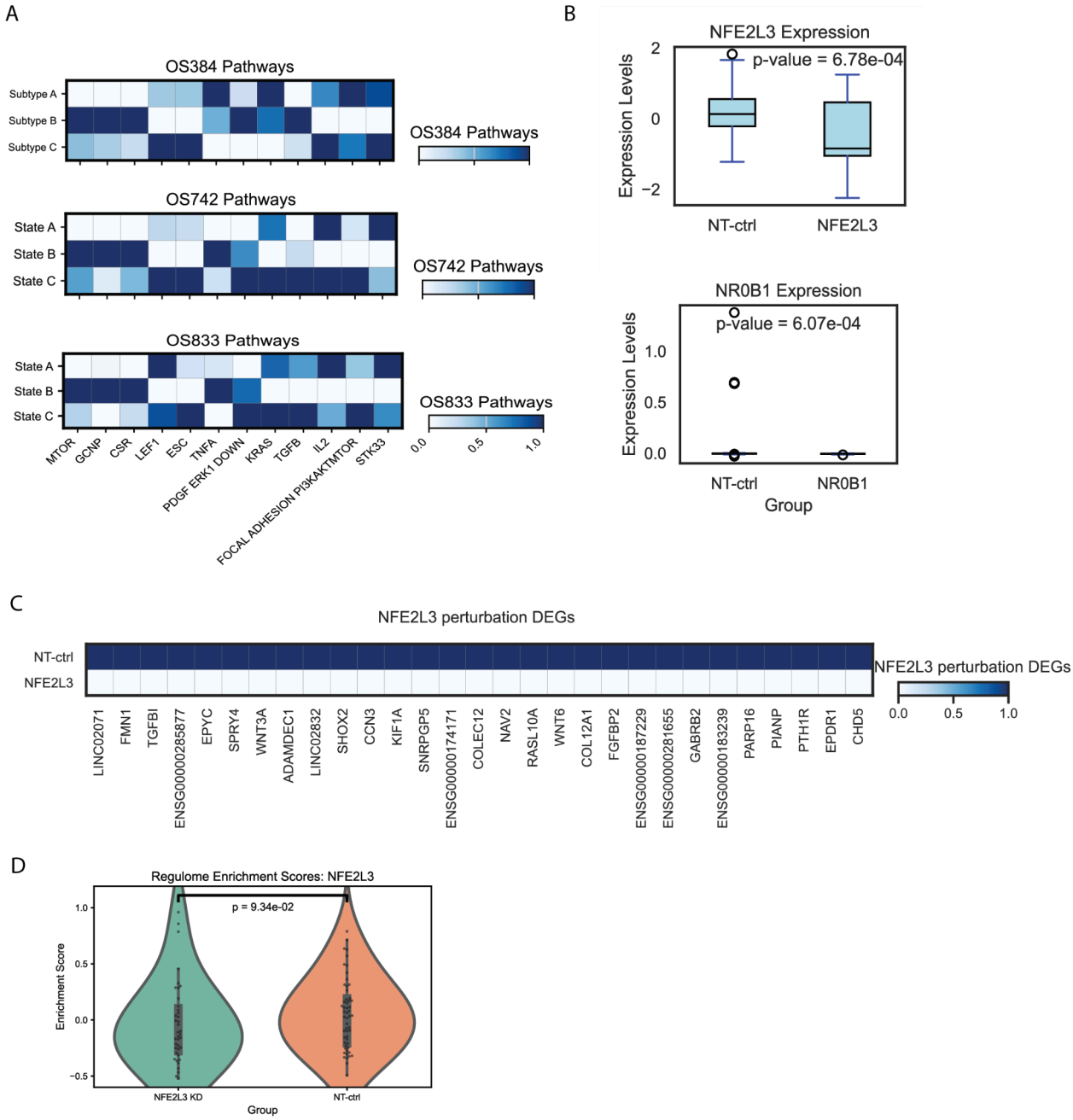


Supplementary Figure 8: Perturb-seq sorting and QC

(A) OS PDX-derived cell lines were transduced with dCas9/CRISPRi KRAB constructs expressing mCherry, sorted based on mCherry and subsequently transduced with dual guide constructs and sorted based on both BFP and mCherry.

(B) Quality control plots for all 3 samples used in the perturb-seq experiment**.** Datasets for OS384, OS742 and OS833 were filtered based on gene counts, mitochondrial percentage and total counts.

Supplemental 9



Supplementary Figure 9: Perturb-seq QC and additional perturb-seq replicate.

(A) Matrix plots representing quantified pathway enrichment in the different states. This analysis was performed on n=3 biological replicates.

(B) Box plot comparing the expression levels of NFE2L3 between non-targeting control (NT-ctrl) and NFE2L3 perturbation groups. The box plot displays the median expression, interquartile range (light blue box), and whiskers representing the data range within 1.5 times the interquartile range. A Mann-Whitney U test was conducted to assess the statistical significance of the difference between the two groups, with the resulting p-value annotated on the plot (p-value = 6.78e-4).

(C) The matrix plot displays differentially expressed genes (DEGs) following NFE2L3 perturbation in the OS833 sample compared to the non-targeting control (NT-ctrl). The heatmap is restricted to significant DEGs with a $\log_2$ fold change > 1 or < -1 and an adjusted p-value < 0.05.

(D) Here, we are plotting the distribution of NFE2L3 regulome enrichment scores in the non-targeting control cells and the NFE2L3 KD cells. Statistical significance was determined using a Mann-Whitney U test.

Tables

Table 1

State	Marker
A	S100A6
A	LGALS3
A	RPL3
A	RPL12
A	RPL10
A	COL1A1
A	COL1A2
B	MCM7
B	CENPF
B	MCM3
B	PCNA
B	TUBB
B	ATAD2
B	CDK1
B	UBE2C
B	RANBP1
B	TUBA1B
B	UBE2T
C	PSMB1
C	FTH1
C	GTF3C6
C	PSMB6